

SEQUENCE LISTING

<110> Sim, Gek-Kee
Yang, Shumin
Dreitz, Matthew J.
Wonderling, Ramani S.

<120> CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF

<130> IM-2-C2

<140> not yet assigned
<141> 1999-12-01

<150> 09/322,409
<151> 1999-05-28

<150> 60/087,306
<151> 1998-05-29

<160> 174

<170> PatentIn Ver. 2.0

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55 60 65

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85 90 95 100

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Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp
105 110 115

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35 40 45

Met Glu Leu Thr Val Lys Asp Val Phe Thr Ala Pro Lys Asn Thr Ser
50 55 60

Asp Lys Glu Ile Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Ile Tyr
65 70 75 80

Thr His Asn Cys Ser Asn Arg Tyr Leu Arg Gly Leu Tyr Arg Asn Leu
85 90 95

Ser Ser Met Ala Asn Lys Thr Cys Ser Met Asn Glu Ile Lys Lys Ser
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Trp	Ser	Pro	Thr	Ala	Ser	Leu	Ser	Pro	Gly							
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ctc	cgc	ggg	acc	ccc	gac	tgc	tcc	ttc	agc	cac	agc	ccc	atc	tcc	tcc	151
Leu	Arg	Gly	Thr	Pro	Asp	Cys	Ser	Phe	Ser	His	Ser	Pro	Ile	Ser	Ser	
25																35
acc	ttc	gcf	gtc	acc	atc	cgc	aag	ctg	tct	gat	tac	ctg	ctt	cag	gac	199
Thr	Phe	Ala	Val	Thr	Ile	Arg	Lys	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	
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tat	cca	gtc	act	gtc	gcc	tcc	aac	ctg	cag	gac	gac	gag	ctc	tgc	ggg	247
Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Asp	Glu	Leu	Cys	Gly	
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gcf	ttc	tgg	cgc	ctg	gtc	ctg	gcc	cag	cgc	tgg	atg	gtg	cgg	ctc	cag	295
Ala	Phe	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Val	Arg	Leu	Gln	
75																85
gct	gtg	gct	gga	tcc	caa	atg	caa	atc	ctg	ctg	gag	gct	gtc	aac	acg	343
Ala	Val	Ala	Gly	Ser	Gln	Met	Gln	Ile	Leu	Leu	Glu	Ala	Val	Asn	Thr	
90																100
gag	ata	cac	ttt	gtc	acc	ttc	tgt	gcc	ttc	cag	ccc	ctc	ccc	agc	tgt	391
Glu	Ile	His	Phe	Val	Thr	Phe	Cys	Ala	Phe	Gln	Pro	Leu	Pro	Ser	Cys	
105																115
ctt	cgc	ttc	gtc	cag	acc	aac	atc	tcc	cac	ctc	ctg	cag	gac	acc	tcc	439
Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	His	Leu	Leu	Gln	Asp	Thr	Ser	
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cag	cag	ctg	gcc	ctg	aag	ccc	tgg	atc	acc	cgc	agg	aat	ttc	tcc	487	
Gln	Gln	Leu	Ala	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Arg	Asn	Phe	Ser	
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Gly	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Val	Pro	
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cca	agg	agc	ccc	ggg	gcc	ctg	gag	gcc	act	gcc	ttg	cca	gcc	cct	cag	583
Pro	Arg	Ser	Pro	Gly	Ala	Leu	Glu	Ala	Thr	Ala	Leu	Pro	Ala	Pro	Gln	
170																180
gca	cct	cgg	ctg	ctc	ctg	ctg	ctg	ccc	gtg	gct	ctc	ctg	ctg			631
Ala	Pro	Arg	Leu	Pro	Val	Ala	Leu	Leu								
185																195

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His Leu Pro Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu	
235 240 245	
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Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly	
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Ser Arg Gln Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro	
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65 70 75 80

Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser Gln Met Gln Ile
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100 105 110

Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115 120 125

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145 150 155 160

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180 185 190

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195 200 205

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245 250 255

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<211> 882

<212> DNA

<213> Canis familiaris

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gtggctgaag gagcagtcgg gggtccgcg gaggccgggg ctgagcagca gcagcagcaa 840
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Primer

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<213> Artificial Sequence

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<213> Artificial Sequence

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Leu Thr Ala Arg Asn Asp Ser Cys Met Glu Leu Thr Val Lys Asp Val
20 25 30

ttc act gct cca aag aac aca agc gat aag gaa atc ttc tgc aga gct 144
Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile Phe Cys Arg Ala
35 40 45

gct act gta ctg cgg cag atc tat aca cac aac tgc tcc aac aga tat 192

Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys Ser Asn Arg Tyr
50 55 60

ctc aga gga ctc tac agg aac ctc agc agc atg gca aac aag acc tgt 240
Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala Asn Lys Thr Cys
65 70 75 80

tct atg aat gaa atc aag aag agt aca ctg aaa gac ttc ttg gaa agg 288
Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp Phe Leu Glu Arg
85 90 95

cta aaa gtg atc atg cag aag aaa tac tac agg cat 324
Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
100 105

<210> 20

<211> 108

<212> PRT

<213> Canis familiaris

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20 25 30

Phe Thr Ala Pro Lys Asn Thr Ser Asp Lys Glu Ile Phe Cys Arg Ala
35 40 45

Ala Thr Val Leu Arg Gln Ile Tyr Thr His Asn Cys Ser Asn Arg Tyr
50 55 60

Leu Arg Gly Leu Tyr Arg Asn Leu Ser Ser Met Ala Asn Lys Thr Cys
65 70 75 80

Ser Met Asn Glu Ile Lys Lys Ser Thr Leu Lys Asp Phe Leu Glu Arg
85 90 95

Leu Lys Val Ile Met Gln Lys Lys Tyr Tyr Arg His
100 105

<210> 21

<211> 324

<212> DNA

<213> Canis familiaris

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<220>
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Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
20 25 30

act gtc gcc tcc aac ctg cag gac gag ctc tgc ggg gcg ttc tgg 144
Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
35 40 45

cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct 192
Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
50 55 60

gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac 240
Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
65 70 75 80

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Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe
85 90 95

gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc cag cag ctg	336		
Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Gln Gln Leu			
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gcc gcc ctg aag ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg	384		
Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu			
115	120	125	
gag ctg cag tgt cag ccc gac tcc tct aca ttg gtg ccc cca agg agc	432		
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser			
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145	150	155	160
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165	170	175	
gcc tgg tgc ctg cat tgg cga agg agg cgg cgg cgg agg tca ccc tac	576		
Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Ser Pro Tyr			
180	185	190	
cct ggg gag cag agg aca ctg agg ccc agc gag cgg agc cat ctg ccc	624		
Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro			
195	200	205	
gag gac aca gag ctg gga cct gga ggg agt cag cta gag act ggt ccc	672		
Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro			
210	215	220	
ttc ctc gac cac gca gcc ccg ctc gct ccc tcc cca gga tca agg caa	720		
Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln			
225	230	235	240
cgc ccg ccc cca acg ccc cca aag cca gcc cca gcc cca cct ctc ccc	768		
Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro			
245	250	255	
ctc tgt aca aag tcc ttg ccc cca aga aat tgt ata	804		
Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile			
260	265		

<210> 23
<211> 268

<212> PRT

<213> Canis familiaris

<400> 23

Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
1 5 10 15

Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
50 55 60

Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
65 70 75 80

Phe Val Thr Phe Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe
85 90 95

Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Gln Gln Leu
100 105 110

Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu
115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser
130 135 140

Pro Gly Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg
145 150 155 160

Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr
165 170 175

Ala Trp Cys Leu His Trp Arg Arg Arg Arg Arg Arg Ser Pro Tyr
180 185 190

Pro Gly Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro
195 200 205

Glu Asp Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro
210 215 220

Phe Leu Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln
225 230 235 240

Arg Pro Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro
245 250 255

Leu Cys Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile
260 265

<210> 24
<211> 804
<212> DNA
<213> Canis familiaris

<400> 24
tataacaattt cttggggca aggacttgtt acagaggggg agaggtgggg ctggggctgg 60
ctttgggggc gttggggcg ggcgttgct tgatcctggg gagggagcga gcggggctgc 120
gtggtcgagg aaggaccag tctctagctg actccctcca ggtcccaagct ctgtgtcctc 180
ggcagatgg ctccgctcgc tgggcctcag tgtcctctgc tccccagggt agggtgacct 240
ccggccgcgc ctccctcgc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300
gggcagcagc agcaggagga gcagccgagg tgcctgaggg gctggcaagg cagtggcctc 360
cagggccccg gggctcccttg ggggcaccaa tgtagaggag tcgggctgac actgcagctc 420
caggcacccg gagaaattcc tgcgggtgat ccaggccttc agggcggcca gctgctggga 480
ggtgtcctgc aggaggtggg agatgttgtt ctggacgaag cgaagacagc tggggagggg 540
ctggaaggca cagaaggta caaagtgtat ctccgtttt acagcctcca gcaggatttg 600
catttggat ccagccacag cctggagccg caccatccag cgctgggcca ggaccaggcg 660
ccagaacgcc ccgcagagct cgtcgccctg caggtggag ggcacagtga ctggatagtc 720
ctgaagcagg taatcagaca gcttgcggat ggtgaccgcg aagggtggagg agatggggct 780
gtggctgaag gagcagtcgg gggt 804

<210> 25
<211> 985
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (74)..(901)

<400> 25
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gcctccggcc gag atg ata gtg ctg gcg cca gcc tgg agc cca act gcc 109
Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Ala
1 5 10
tcc ctg ttg ctg ctg ctg ctc agc ccc ggc ctc cgc ggg acc ccc 157
Ser Leu Leu Leu Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro
15 20 25
gac tgc tcc ttc agc cac agc ccc atc tcc tcc acc ttc gcg gtc acc 205
Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr
30 35 40
atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc act gtc 253
Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val
45 50 55 60
gcc tcc aac ctg cag gac gag ctc tgc ggg gcg ttc tgg cgc ctg 301
Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu
65 70 75
gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct gga tcc 349
Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser
80 85 90
caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac ttt gtc 397
Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val
95 100 105
acc ttc tgt gcc ttc cag gac acc tcc cag cag ctg gcc gcc ctg aag 445
Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys
110 115 120
ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg gag ctg cag tgt 493
Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys
125 130 135 140
cag ccc gac tcc tct aca ttg gtg ccc cca agg agc ccc ggg gcc ctg 541
Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu
145 150 155
gag gcc act gcc ttg cca gcc cct cag gca cct cgg ctg ctc ctc ctg 589

Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu				
160	165	170		
ctg ctg ctg ccc gtg gct ctc ctg ctg atg tcc act gcc tgg tgc ctg	637			
Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu				
175	180	185		
cat tgg cga agg agg cgg cgg agg tca ccc tac cct ggg gag cag	685			
His Trp Arg Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln				
190	195	200		
agg aca ctg agg ccc agc gag cgg agc cat ctg ccc gag gac aca gag	733			
Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu				
205	210	215	220	
ctg gga cct gga ggg agt cag cta gag act ggt ccc ttc ctc gac cac	781			
Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His				
225	230	235		
gca gcc ccg ctc gct ccc tcc cca gga tca agg caa cgc ccg ccc cca	829			
Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro				
240	245	250		
acg ccc cca aag cca gcc cca gcc cca cct ctc ccc ctc tgt aca aag	877			
Thr Pro Pro Lys Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys				
255	260	265		
tcc ttg ccc cca aga aat tgt ata taaatcatcc ttttctacca gaaaaaaaaa	931			
Ser Leu Pro Pro Arg Asn Cys Ile				
270	275			
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa	985			

<210> 26
<211> 276
<212> PRT
<213> Canis familiaris

<400> 26
Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Ala Ser Leu Leu
1 5 10 15

Leu Leu Leu Ser Pro Gly Leu Arg Gly Thr Pro Asp Cys Ser Phe
20 25 30

Ser His Ser Pro Ile Ser Ser Thr Phe Ala Val Thr Ile Arg Lys Leu
35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60

Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp Arg Leu Val Leu Ala Gln
65 70 75 80

Arg Trp Met Val Arg Leu Gln Ala Val Ala Gly Ser Gln Met Gln Ile
85 90 95

Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Phe Cys Ala
100 105 110

Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala Leu Lys Pro Trp Ile Thr
115 120 125

Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
130 135 140

Ser Thr Leu Val Pro Pro Arg Ser Pro Gly Ala Leu Glu Ala Thr Ala
145 150 155 160

Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu Leu Leu Leu Pro
165 170 175

Val Ala Leu Leu Leu Met Ser Thr Ala Trp Cys Leu His Trp Arg Arg
180 185 190

Arg Arg Arg Arg Ser Pro Tyr Pro Gly Glu Gln Arg Thr Leu Arg
195 200 205

Pro Ser Glu Arg Ser His Leu Pro Glu Asp Thr Glu Leu Gly Pro Gly
210 215 220

Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu Asp His Ala Ala Pro Leu
225 230 235 240

Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro Pro Pro Thr Pro Pro Lys
245 250 255

Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys Thr Lys Ser Leu Pro Pro
260 265 270

Arg Asn Cys Ile
275

<211> 985

<212> DNA

<213> Canis familiaris

<400> 27

ttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60

ttgctggtag aaaaggatga tttatataca atttcttggg ggcaaggact ttgtacagag 120

ggggagaggt ggggctgggg ctggcttgg gggcggtggg ggcgggcgtt gccttgatcc 180

tggggaggga gcgagcgggg ctgcgtggc gaggaaggga ccagtctcta gctgactccc 240

tccaggtccc agctctgtgt cctcgggcag atggctccgc tcgctgggcc tcagtgtcct 300

ctgctccccca ggttagggtg acctccgccc ccgcctcctt cgccaatgca ggcaccaggc 360

agtggacatc agcaggagag ccacgggcag cagcagcagg aggagcagcc gaggtgcctg 420

aggggctggc aaggcagtgg cctccaggc cccggggctc cttggggca ccaatgtaga 480

ggagtcgggc tgacactgca gctccaggca cccggagaaa ttccctgcggg tgatccagg 540

cttcagggcg gccagctgct gggaggtgtc ctggaaaggca cagaaggtaa caaaagtgtat 600

ctccgtgttg acagcctcca gcaggatttgcatttggat ccagccacag cctggagccg 660

caccatccag cgctgggcca ggaccaggcg ccagaacgcc ccgcagagct cgtcgccctg 720

caggttggag ggcacagtga ctggatagtc ctgaaggcagg taatcagaca gcttgcggat 780

ggtgaccgcg aagggtggagg agatggggct gtggctgaag gagcagtcgg gggtccgcg 840

gaggccgggg ctgagcagca gcagcagcaa cagggaggca gttggctcc aggctggcgc 900

cagcactatc atctcgcccg gaggcccctc atgcctatgg tcagatcagg cttgccccag 960

ctggcgtgg aaggggccag gccgg 985

<210> 28

<211> 828

<212> DNA

<213> Canis familiaris

<400> 28

atgatagtgcc tggcgccagc ctggagccca actgcctccc tggctgtgtc gctgctgctc 60

agccccggcc tccgcgggac ccccactgc tccttcagcc acagccccat ctccctccacc 120
ttcgcggtaa ccatccgcaa gctgtctgat tacctgcttc aggactatcc agtcaactgtc 180
gcctccaacc tgcaggacga cgagctctgc gggcggttct ggccgcctggc cctggcccaag 240
cgctggatgg tgcggctcca ggctgtggct ggatccaaa tgcaaattct gctggaggct 300
gtcaacacgg agatacacatt tgcaccccttc tgccttcaggacacccctc ccagcagctg 360
gccgcctga agccctggat cacccgcagg aatttctccg ggtgcctgga gctgcagtgt 420
cagccccact cctctacatt ggtgccttccaggagccccggccgcctgga ggccactgccc 480
ttgccagccc ctcaggcacc tcggctgctc ctcctgctgc tgctgcccgt ggctctcctg 540
ctgatgtcca ctgcctggtg cctgcattgg cgaaggaggc ggcggcggag gtcaccctac 600
cctggggagc agaggacact gaggcccagc gagcggagcc atctgcccga ggacacagag 660
ctgggacctg gagggagtca gctagagact ggtcccttcc tcgaccacgc agcccccgtc 720
gctccctccc caggatcaag gcaacgccccggccgccttccggccgcctgga ggccactgccc 780
ccacctctcc ccctctgtac aaagtccttg ccccaagaa attgtata 828

<210> 29
<211> 828
<212> DNA
<213> Canis familiaris

<400> 29
tatacaattt ctgggggca aggactttgt acagaggggg agaggtgggg ctggggctgg 60
ctttggggc gttggggcg ggcgttgct tgatccctggg gagggagcga gcggggctgc 120
gtggtcgagg aagggaccag tctctagctg actccctcca ggtcccagct ctgtgtcctc 180
gggcagatgg ctccgctcgc tgggcctcag tgcctctgc tcccccagggt agggtgacct 240
ccggcccccgc ctccttcgccc aatgcaggca ccaggcagtg gacatcagca ggagagccac 300
gggcagcagc agcaggagga gcagccgagg tgcctgaggg gctggcaagg cagtggcctc 360
cagggccccg gggctcccttg ggggcaccaa tgtagaggag tcgggctgac actgcagctc 420
caggcaccccg gagaaattcc tgcgggtgat ccaggcgttc agggcggcca gctgctggga 480

ggtgtcctgg aaggcacaga aggtgacaaa gtgtatctcc gtgttgacag cctccagcag 540
gatttgcatt tggatccag ccacagcctg gagccgcacc atccagcgct gggccaggac 600
caggcgccag aacgccccgc agagctcgtc gtcctgcagg ttggaggcga cagtgactgg 660
atagtccctga agcaggtaat cagacagctt gcggatggtg accgcgaagg tggaggagat 720
ggggctgtgg ctgaaggagc agtcgggggt cccgcggagg ccggggctga gcagcagcag 780
cagcaacagg gaggcagttg ggctccaggc tggcgccagc actatcat 828

<210> 30
<211> 750
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(750)

<400> 30
acc ccc gac tgc tcc ttc agc cac agc ccc atc tcc tcc acc ttc gcg 48
Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala
1 5 10 15

gtc acc atc cgc aag ctg tct gat tac ctg ctt cag gac tat cca gtc 96
Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
20 25 30

act gtc gcc tcc aac ctg cag gac gag ctc tgc ggg gcg ttc tgg 144
Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
35 40 45

cgc ctg gtc ctg gcc cag cgc tgg atg gtg cgg ctc cag gct gtg gct 192
Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
50 55 60

gga tcc caa atg caa atc ctg ctg gag gct gtc aac acg gag ata cac 240
Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
65 70 75 80

ttt gtc acc ttc tgt gcc ttc cag gac acc tcc cag cag ctg gcc gcc 288
Phe Val Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala
85 90 95

ctg aag ccc tgg atc acc cgc agg aat ttc tcc ggg tgc ctg gag ctg	336
Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu	
100 105 110	
cag tgt cag ccc gac tcc tct aca ttg gtg ccc cca agg agc ccc ggg	384
Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly	
115 120 125	
gcc ctg gag gcc act gcc ttg cca gcc cct cag gca cct cgg ctg ctc	432
Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu	
130 135 140	
ctc ctg ctg ctg ccc gtg gct ctc ctg atg tcc act gcc tgg	480
Leu Leu Leu Leu Pro Val Ala Leu Leu Met Ser Thr Ala Trp	
145 150 155 160	
tgc ctg cat tgg cga agg agg cgg cgg cgg agg tca ccc tac cct ggg	528
Cys Leu His Trp Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly	
165 170 175	
gag cag agg aca ctg agg ccc agc gag cgg agc cat ctg ccc gag gac	576
Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp	
180 185 190	
aca gag ctg gga cct gga ggg agt cag cta gag act ggt ccc ttc ctc	624
Thr Glu Leu Gly Pro Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu	
195 200 205	
gac cac gca gcc ccg ctc gct ccc tcc cca gga tca agg caa cgc ccg	672
Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro	
210 215 220	
ccc cca acg ccc cca aag cca gcc cca gcc cct ctc ccc ctc tgt	720
Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys	
225 230 235 240	
aca aag tcc ttg ccc cca aga aat tgt ata	750
Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile	
245 250	

<210> 31
 <211> 250
 <212> PRT
 <213> Canis familiaris

<400> 31
 Thr Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Ala

1

5

10

15

Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Ala Phe Trp
35 40 45

Arg Leu Val Leu Ala Gln Arg Trp Met Val Arg Leu Gln Ala Val Ala
50 55 60

Gly Ser Gln Met Gln Ile Leu Leu Glu Ala Val Asn Thr Glu Ile His
65 70 75 80

Phe Val Thr Phe Cys Ala Phe Gln Asp Thr Ser Gln Gln Leu Ala Ala
85 90 95

Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu
100 105 110

Gln Cys Gln Pro Asp Ser Ser Thr Leu Val Pro Pro Arg Ser Pro Gly
115 120 125

Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Arg Leu Leu
130 135 140

Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Thr Ala Trp
145 150 155 160

Cys Leu His Trp Arg Arg Arg Arg Arg Ser Pro Tyr Pro Gly
165 170 175

Glu Gln Arg Thr Leu Arg Pro Ser Glu Arg Ser His Leu Pro Glu Asp
180 185 190

Thr Glu Leu Gly Pro Gly Gly Ser Gln Leu Glu Thr Gly Pro Phe Leu
195 200 205

Asp His Ala Ala Pro Leu Ala Pro Ser Pro Gly Ser Arg Gln Arg Pro
210 215 220

Pro Pro Thr Pro Pro Lys Pro Ala Pro Ala Pro Pro Leu Pro Leu Cys
225 230 235 240

Thr Lys Ser Leu Pro Pro Arg Asn Cys Ile
245 250

<210> 32

<211> 750

<212> DNA

<213> Canis familiaris

<400> 32

tatacaattt cttgggggca aggactttgt acagaggggg agaggtgggg ctggggctgg 60

ctttgggggc gttgggggca ggcgttgct tgatcctggg gagggagcga gcggggctgc 120

gtggtcgagg aagggaccag tctctagctg actccctcca ggtcccaagct ctgtgtcctc 180

gggcagatgg ctccgctcgc tgggcctcag tgtcctctgc tccccagggt agggtgacct 240

ccggccgcccgc ctccctcgcc aatgcaggca ccaggcagtgc gacatcagca ggagagccac 300

gggcagcagc agcaggagga gcagccgagg tgcctgaggg gctggcaagg cagtggcctc 360

cagggccccg gggctcccttg ggggcaccaa tgtagaggag tcgggctgac actgcagctc 420

caggcacccg gagaaattcc tgcgggtgat ccagggcttc agggcggcca gctgctggga 480

ggtgtcctgg aaggcacaga aggtgacaaa gtgtatctcc gtgttgacag cctccagcag 540

gatttgcat tggatccag ccacagcctg gagccgcacc atccagcgtc gggccaggac 600

caggcgccag aacgccccgc agagctcgtc gtcctgcagg ttggaggcga cagtgactgg 660

atagtcctga agcaggtaat cagacagctt gcggatggtg accgcgaagg tggaggagat 720

ggggctgtgg ctgaaggagc agtcgggggt 750

<210> 33

<211> 1019

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (74)..(166)

<400> 33

ccggcctggc cccttccacg cccagctggg gcaagcctga tctgaccata ggcattgggg 60

gcctccggcc gag atg ata gtg ctg gcg cca gcc tgg agc cca act gtg 109

Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Val

1

5

10

cgt ata ccc ggg gga caa ggc ggg gga cag gca gag cgc tac cga gct 157
Arg Ile Pro Gly Gly Gln Gly Gly Gln Ala Glu Arg Tyr Arg Ala
15 20 25

ggg cag agc tgagagagca gacggacaga ggctccctg ttgctgctgc 206
Gly Gln Ser
30

tgctgctcag cccggccctc cgccggaccc ccgactgctc cttcagccac agccccatct 266
cctccacctt cgccgtcacc atccgcaagc tgtctgatta cctgcttcag gactatccag 326
tcactgtcgc ctccaacctg caggacgacg agctctgcgg ggcgttctgg cgccctggcc 386
tggcccagcg ctggatggtg cggctccagg ctgtggctgg atcccaaatg caaatcctgc 446
tggaggctgt caacacggag atacactttg tcaccccttg tgcccttccag gacacccccc 506
agcagctggc cgccctgaag ccctggatca cccgcaggaa tttctccggg tgcctggagc 566
tgcagtgtca gcccgactcc tctacattgg tgcccccaag gagccccggg gccctggagg 626
ccactgcctt gccagccctt caggcacctc ggctgctcct cctgctgctg ctgcccgtgg 686
ctctcctgct gatgtccact gcctggtgcc tgcattggcg aaggaggcgg cggcggaggt 746
caccctaccc tggggagcag aggacactga ggcccagcga gcggagccat ctgcccggagg 806
acacagagct gggacctgga gggagtcagc tagagactgg tcccttcctc gaccacgcag 866
ccccgctcgc tccctccccca ggtcaaggc aacgccccgc cccaaacgccc ccaaagccag 926
ccccagcccc acctctcccc ctctgtacaa agtccttgcc cccaaagaaat tgtatataaa 986

tcatcctttt ctacaaaaaa aaaaaaaaaa aaa 1019

<210> 34
<211> 31
<212> PRT
<213> Canis familiaris

<400> 34
Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Val Arg Ile Pro Gly
1 5 10 15
Gly Gln Gly Gly Gln Ala Glu Arg Tyr Arg Ala Gly Gln Ser

20

25

30

<210> 35

<211> 1019

<212> DNA

<213> Canis familiaris

<400> 35

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actttgtaca gagggggaga ggtggggctg gggctggctt tgggggcgtt gggggcgggc 120

gttgccttga tcctggggag ggagcgagcg gggctgcgtg gtcgaggaag ggaccagtct 180

ctagctgact ccctccaggt cccagctctg tgtcctcggg cagatggctc cgctcgctgg 240

gcctcagtgt cctctgctcc ccaggtagg gtgacactccg ccgcccctc cttcgccaat 300

gcagggacca ggcagtggac atcagcagga gagccacggg cagcagcagc aggaggagca 360

gccgaggtgc ctgaggggct ggcaaggcag tggcctccag ggccccgggg ctccttgggg 420

gcaccaatgt agaggagtcg ggctgacact gcagctccag gcacccggag aaattcctgc 480

gggtgatcca gggcttcagg gcggccagct gctggaggt gtcctggaag gcacagaagg 540

tgacaaagtg tatctccgtg ttgacagcct ccagcaggat ttgcatttgg gatccagcca 600

cagcctggag ccgcaccatc cagcgctggg ccaggaccag gcgccagaac gccccgcaga 660

gctcgctgtc ctgcagggtt gaggcgacag tgactggata gtcctgaagc aggtaatcag 720

acagcttgcg gatggtgacc gcgaaaggtagg aggagatggg gctgtggctg aaggagcagt 780

cgggggtccc gcggaggccg gggctgagca gcagcagcag caacagggag gcctctgtcc 840

gtctgctctc tcaagctctgc ccagctcggt agcgctctgc ctgtcccccg cttgtcccc 900

cgggtatacg cacagttggg ctccaggctg gcgccagcac tatcatctcg gccggaggcc 960

cctcatgcct atggtcagat caggcttgc ccagctggc gtggaaagggg ccaggccgg 1019

<210> 36

<211> 93

<212> DNA

<213> Canis familiaris

<400> 36
atgatagtgc tggcgccagc ctggagccca actgtgcgta taccgggggg acaaggcg 60
ggacaggcag agcgctaccg agctgggcag agc 93

<210> 37
<211> 93
<212> DNA
<213> Canis familiaris

<400> 37
gctctgcccc gctcggttagc gctctgcctg tccccccctt tgtccccccgg gtatacgac 60
agttgggctc caggctggcg ccagcactat cat 93

<210> 38
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 38
tgaattcgga cataacttca atattac 27

<210> 39
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 39

tctcgagatt cagcttcaat gcctgta 27

<210> 40
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 40

cccaagctta tgggtctcac ctcccaac

28

<210> 41

<211> 395

<212> DNA

<213> Felis catus

<400> 41

ggccataggc atgaagggcc tccggccgag atgatagtgc tggcgccagc ctggagccca 60

actacctccc tgctgctgct gctactgctc agccctggcc tccgcgggtc ccccgactgt 120

tccttcagcc acagccccat ctccctccacc ttcaaggtca ccattccaaa gctgtctgtat 180

tacctgcttc aggattaccc agtcaccgtc gcctccaacc tacaggacga cgagctctgt 240

ggccattctt ggcacctggc cctggccag cgctggatgg gtcggctcaa ggctgtggct 300

gggtcccaga tgcaaagcct gctggaggcg gtcaacaccc agatacattt tgtcaccttg 360

tgtgccttccc agccctccc cagctgtctt cgatt 395

<210> 42

<211> 793

<212> DNA

<213> Felis catus

<400> 42

cttcaagggtc accatccgaa agctgtctga ttacctgctt caggattacc cagtcaccgt 60

cgccctccaac ctacaggacg acgagctctg tggccatcc tggcacctgg tcctggccca 120

gcgcgtggatg ggtcggtca aggctgtggc tgggtcccag atgcaaagcc tgctggaggc 180

ggtcaacacc gagatacatt ttgtcacctt gtgtgccttc cagccctcc ccagctgtct 240

tcgattcgtc cagaccaaca tctcccacct cctgcaggac acctccgagc agctggcgcc 300

cttgaagccc tggatcaccc gcaggaattt ctcgggggtgc ctggagctac agtgtcagcc 360

cgactcctcc accccactgc ccccaaggag ccccagggcc ttggaggcca cagccctgcc 420
agcccctcag gcccctctgc tgctcctcct gctgctgttgc cctgtggctc tcttgctgat 480
gtccgcccgc tggcctgc actggcgaag aaggagatgg agaacgcctt accccaggga 540
gcagaggaag acactgaggc ccagagagag gaatcacctg cccgaggaca cagagccggg 600
actcggagaa agtcagctag agactggttc cttcctcgac cacgctgccc cgctcactct 660
ccccccggga tggaggcaac gccagccccc aacgccagcc ccagaccac ctatccccct 720
ctgtacaaag tccttgcct cagaaatttgc tatataaattc atcctttctt accaaaaaaaaa 780
aaaaaaaaaaa aaa 793

<210> 43
<211> 942
<212> DNA
<213> *Felis catus*

<220>
<221> CDS
<222> (31)..(903)

<400> 43

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Met Ile Val Leu Ala Pro Ala Trp
1 5

agc cca act acc tcc ctg ctg ctg cta ctg ctc agc cct ggc ctc 102
Ser Pro Thr Thr Ser Leu Leu Leu Leu Leu Leu Ser Pro Gly Leu
10 15 20

cgc ggg tcc ccc gac tgt tcc ttc agc cac agc ccc atc tcc tcc acc 150
Arg Gly Ser Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr
25 30 35 40

ttc aag gtc acc atc cga aag ctg tct gat tac ctg ctt cag gat tac 198
Phe Lys Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
45 50 55

cca gtc acc gtc gcc tcc aac cta cag gac gac gag ctc tgt ggg cca 246
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Pro
60 65 70

ttc tgg cac ctg gtc ctg gcc cag cgc tgg atg ggt cgg ctc aag gct 294

Phe	Trp	His	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Gly	Arg	Leu	Lys	Ala	
75																85
gtg gct ggg tcc cag atg caa agc ctg ctg gag gcg gtc aac acc gag															342	
Val	Ala	Gly	Ser	Gln	Met	Gln	Ser	Leu	Leu	Glu	Ala	Val	Asn	Thr	Glu	
90																100
ata cat ttt gtc acc ttg tgt gcc ttc cag ccc ctc ccc agc tgt ctt															390	
Ile	His	Phe	Val	Thr	Leu	Cys	Ala	Phe	Gln	Pro	Leu	Pro	Ser	Cys	Leu	
105																110
cga ttc gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc gag															438	
Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	His	Leu	Leu	Gln	Asp	Thr	Ser	Glu	
125																130
cag ctg gcg gcc ttg aag ccc tgg atc acc cgc agg aat ttc tcg ggg															486	
Gln	Leu	Ala	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Arg	Asn	Phe	Ser	Gly	
140																145
tgc ctg gag cta cag tgt cag ccc gac tcc tcc acc cca ctg ccc cca															534	
Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Pro	Leu	Pro	Pro	
155																160
agg agc ccc agg gcc ttg gag gcc aca gca gcc ctg cca gcc cct cag gcc															582	
Arg	Ser	Pro	Arg	Ala	Leu	Glu	Ala	Thr	Ala	Leu	Pro	Ala	Pro	Gln	Ala	
170																175
cct ctg ctg ctc ctc ctg ctg ttg cct gtg gct ctc ttg ctg atg															630	
Pro	Leu	Pro	Val	Ala	Leu	Leu	Met									
185																190
tcc gcc gcc tgg tgc ctg cac tgg cga aga agg aga tgg aga acg ccc															678	
Ser	Ala	Ala	Trp	Cys	Leu	His	Trp	Arg	Arg	Arg	Trp	Arg	Thr	Pro		
205																210
tac ccc agg gag cag agg aag aca ctg agg ccc aga gag agg aat cac															726	
Tyr	Pro	Arg	Glu	Gln	Arg	Lys	Thr	Leu	Arg	Pro	Arg	Glu	Arg	Asn	His	
220																225
ctg ccc gag gac aca gag ccg gga ctc gga gaa agt cag cta gag act															774	
Leu	Pro	Glu	Asp	Thr	Glu	Pro	Gly	Leu	Gly	Glu	Ser	Gln	Leu	Glu	Thr	
235																240
ggc tcc ttc ctc gac cac gct gcc ccg ctc act ctc ccc ccg gga tgg															822	
Gly	Ser	Phe	Leu	Asp	His	Ala	Ala	Pro	Leu	Thr	Leu	Pro	Pro	Gly	Trp	
250																255
agg caa cgc cag ccc cca acg cca gcc cca gac cca cct atc ccc ctc															870	

Arg Gln Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu
265 270 275 280

tgt aca aag tcc ttg tcc tca gga aat tgt ata taaatcatcc ttttctacca 923
Cys Thr Lys Ser Leu Ser Ser Gly Asn Cys Ile
285 290

aaaaaaaaaaaa aaaaaaaaaa 942

<210> 44
<211> 291
<212> PRT
<213> Felis catus

<400> 44
Met Ile Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Ser Leu Leu Leu
1 5 10 15

Leu Leu Leu Ser Pro Gly Leu Arg Gly Ser Pro Asp Cys Ser Phe
20 25 30

Ser His Ser Pro Ile Ser Ser Thr Phe Lys Val Thr Ile Arg Lys Leu
35 40 45

Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
50 55 60

Gln Asp Asp Glu Leu Cys Gly Pro Phe Trp His Leu Val Leu Ala Gln
65 70 75 80

Arg Trp Met Gly Arg Leu Lys Ala Val Ala Gly Ser Gln Met Gln Ser
85 90 95

Leu Leu Glu Ala Val Asn Thr Glu Ile His Phe Val Thr Leu Cys Ala
100 105 110

Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
115 120 125

His Leu Leu Gln Asp Thr Ser Glu Gln Leu Ala Ala Leu Lys Pro Trp
130 135 140

Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu Glu Leu Gln Cys Gln Pro
145 150 155 160

Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser Pro Arg Ala Leu Glu Ala
165 170 175

Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu Leu Leu Leu Leu Leu
180 185 190

Leu Pro Val Ala Leu Leu Leu Met Ser Ala Ala Trp Cys Leu His Trp
195 200 205

Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro Arg Glu Gln Arg Lys Thr
210 215 220

Leu Arg Pro Arg Glu Arg Asn His Leu Pro Glu Asp Thr Glu Pro Gly
225 230 235 240

Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser Phe Leu Asp His Ala Ala
245 250 255

Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln Arg Gln Pro Pro Thr Pro
260 265 270

Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr Lys Ser Leu Ser Ser Gly
275 280 285

Asn Cys Ile
290

<210> 45

<211> 942

<212> DNA

<213> Felis catus

<400> 45

ttttttttt tttttttttt ggtagaaaaag gatgatttat atacaatttc ctgaggacaa 60

ggactttgtt cagagggggat taggtgggtc tggggctggc gttggggctt ggcgttgctt 120

ccatcccggtt gggagagtgtt gcgccccgtt gtggtcgagg aaggaaccat tctcttagctt 180

actttctccgtt agtcccggtt ctgtgtccctt gggcaggtgtt ttcctctctt tgggccttcag 240

tgtcttccttc tgcctccctttt ggttagggcgtt tctccatctt cttcttcgtt agtgcaggca 300

ccaggcggcg gacatcagca agagagccac aggcaacatc agcaggagga gcagcagagg 360

ggcctgaggg gctggcaggg ctgtggcttc caaggccctt gggctcctt gggcagtgg 420

ggtagggaggat tcgggctgac actgttagctt caggcacccca gagaaattcc tgcgggttat 480

ccagggcttc aaggccgcca gctgctcgga ggtgtcctgc aggaggtggg agatgttgg 540
ctggacgaat cgaagacagc tggggagggg ctggaaggca cacaaggta caaaatgtat 600
ctcggtgttg accgcctcca gcaggcttg catctggac ccagccacag ccttgagccg 660
acccatccag cgctggcca ggaccaggtg ccagaatggc ccacagagct cgtcgtcctg 720
taggttggag ggcacggta ctggtaatc ctgaagcagg taatcagaca gcttcggat 780
ggtgaccttg aaggtggagg agatggggct gtggctgaag gaacagtcgg gggacccgcg 840
gaggccaggg ctgagcagta gcagcagcag cagggaggta gttggctcc aggctggcgc 900
cagcactatc atctcgccg gaggcccttc atgcctatgg cc 942

<210> 46
<211> 873
<212> DNA
<213> *Felis catus*

<400> 46
atgatagtgc tggcgccagc ctggagccca actacccc tgcgtctgct gctactgctc 60
agccctggcc tccgcgggtc ccccgactgt tccttcagcc acagcccat ctccctccacc 120
ttcaaggtca ccatccgaaa gctgtctgat tacctgcttc aggattaccc agtcaccgtc 180
gcctccaacc tacaggacga cgagctctgt gggccattct ggcacctggc cctggcccg 240
cgctggatgg gtcggctcaa ggctgtggct gggtcccaga tgcaaaggct gctggaggcg 300
gtcaacacccg agatacattt tgcaccccttgc tgccttcc agccctccc cagctgtctt 360
cgattcgtcc agaccaacat ctcccaccc tcgcaggaca cctccgagca gctggccggcc 420
ttgaagccct ggatcaccccg caggaatttc tcggggtgcc tggagctaca gtgtcagccc 480
gactcctcca ccccactgcc cccaaaggagc cccagggct tggaggccac agccctgcca 540
gcccctcagg cccctctgt gtccttcctg. ctgcgtttgc ctgtggctct ctgtgtatg 600
tccggccgcct ggtgcctgca ctggcgaaga aggagatgga gaacgcctta ccccaaggag 660
cagaggaaga cactgaggcc cagagagagg aatcacctgc ccgaggacac agagccggga 720
ctcggagaaa gtcagctaga gactggttcc ttcctcgacc acgctgcccc gctcaactctc 780

ccccccggat ggaggcaacg ccagccccca acggcagccc cagaccacc tatccccctc 840

tgtacaaagt cttgtcctc aggaaattgt ata 873

<210> 47

<211> 873

<212> DNA

<213> *Felis catus*

<400> 47

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cgttgggggc tggcggtgcc tccatcccg ggggagagtg agcggggcag cgtggtcgag 120

gaaggaacca gtctctagct gactttctcc gagtcccgcc tctgtgtcct cggcaggtg 180

attcctctct ctgggcctca gtgtcttcct ctgctccctg gggtagggcg ttctccatct 240

ccttcttcgc cagtgcaggc accaggcgcc ggacatcagc aagagagcca caggcaacag 300

cagcaggagg agcagcagag gggcctgagg ggctggcagg gctgtggcct ccaaggccct 360

ggggctcctt ggggcagtg gggtaggaga gtcgggctga cactgttagct ccaggcaccc 420

cgagaaattc ctgcgggtga tccaggcctt caaggccgcc agctgctcgg aggtgtcctg 480

caggaggtgg gagatgttgg tctggacgaa tcgaagacag ctggggaggg gctggaaggc 540

acacaagggtg acaaaatgta tctcggttt gaccgcctcc agcaggctt gcatctggga 600

cccagccaca gccttgagcc gacccatcca gcgctggcc aggaccaggt gccagaatgg 660

cccacagagc tcgtcgtcct gtaggttgg ggcgacggtg actggtaat cctgaagcag 720

gtaatcagac agcttcgga tggtgacctt gaaggtggag gagatggggc tgtggctgaa 780

ggaacagtcg ggggacccgc ggaggccagg gctgagcagt agcagcagca gcagggaggt 840

agttgggctc caggctggcg ccagcactat cat 873

<210> 48

<211> 795

<212> DNA

<213> *Felis catus*

<220>
<221> CDS
<222> (1)..(795)

<400> 48
tcc ccc gac tgt tcc ttc agc cac agc ccc atc tcc tcc acc ttc aag 48
Ser Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Lys
1 5 10 15

gtc acc atc cga aag ctg tct gat tac ctg ctt cag gat tac cca gtc 96
Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
20 25 30

acc gtc gcc tcc aac cta cag gac gag ctc tgt ggg cca ttc tgg 144
Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Pro Phe Trp
35 40 45

cac ctg gtc ctg gcc cag cgc tgg atg ggt cggt ctc aag gct gtg gct 192
His Leu Val Leu Ala Gln Arg Trp Met Gly Arg Leu Lys Ala Val Ala
50 55 60

ggg tcc cag atg caa agc ctg ctg gag gcg gtc aac acc gag ata cat 240
Gly Ser Gln Met Gln Ser Leu Leu Glu Ala Val Asn Thr Glu Ile His
65 70 75 80

ttt gtc acc ttg tgt gcc ttc cag ccc ctc ccc agc tgt ctt cga ttc 288
Phe Val Thr Leu Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe
85 90 95

gtc cag acc aac atc tcc cac ctc ctg cag gac acc tcc gag cag ctg 336
Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Glu Gln Leu
100 105 110

gcg gcc ttg aag ccc tgg atc acc cgc agg aat ttc tcg ggg tgc ctg 384
Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu
115 120 125

gag cta cag tgt cag ccc gac tcc tcc acc cca ctg ccc cca agg agc 432
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser
130 135 140

ccc agg gcc ttg gag gcc aca gcc ctg cca gcc cct cag gcc cct ctg 480
Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu
145 150 155 160

ctg ctc ctc ctg ctg ttg cct gtg gct ctc ttg ctg atg tcc gcc 528
Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Met Ser Ala
165 170 175

gcc tgg tgc ctg cac tgg cga aga agg aga tgg aga acg ccc tac ccc 576
 Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro
 180 185 190

agg gag cag agg aag aca ctg agg ccc aga gag agg aat cac ctg ccc 624
 Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His Leu Pro
 195 200 205

gag gac aca gag ccg gga ctc gga gaa agt cag cta gag act ggt tcc 672
 Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser
 210 215 220

ttc ctc gac cac gct gcc ccg ctc act ctc ccc ccg gga tgg agg caa 720
 Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln
 225 230 235 240

cgc cag ccc cca acg cca gcc cca gac cca cct atc ccc ctc tgt aca 768
 Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Ile Pro Leu Cys Thr
 245 250 255

aag tcc ttg tcc tca gga aat tgt ata 795
 Lys Ser Leu Ser Ser Gly Asn Cys Ile
 260 265

<210> 49
 <211> 265
 <212> PRT
 <213> Felis catus

<400> 49
 Ser Pro Asp Cys Ser Phe Ser His Ser Pro Ile Ser Ser Thr Phe Lys
 1 5 10 15

Val Thr Ile Arg Lys Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val
 20 25 30

Thr Val Ala Ser Asn Leu Gln Asp Asp Glu Leu Cys Gly Pro Phe Trp
 35 40 45

His Leu Val Leu Ala Gln Arg Trp Met Gly Arg Leu Lys Ala Val Ala
 50 55 60

Gly Ser Gln Met Gln Ser Leu Leu Glu Ala Val Asn Thr Glu Ile His
 65 70 75 80

Phe Val Thr Leu Cys Ala Phe Gln Pro Leu Pro Ser Cys Leu Arg Phe

85

90

95

Val Gln Thr Asn Ile Ser His Leu Leu Gln Asp Thr Ser Glu Gln Leu
100 105 110

Ala Ala Leu Lys Pro Trp Ile Thr Arg Arg Asn Phe Ser Gly Cys Leu
 115 120 125

Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Pro Leu Pro Pro Arg Ser
130 135 140

Pro Arg Ala Leu Glu Ala Thr Ala Leu Pro Ala Pro Gln Ala Pro Leu
145 150 155 160

Leu Leu Leu Leu Leu Leu Leu Pro Val Ala Leu Leu Leu Leu Met Ser Ala
165 170 175

Ala Trp Cys Leu His Trp Arg Arg Arg Arg Trp Arg Thr Pro Tyr Pro
180 185 190

Arg Glu Gln Arg Lys Thr Leu Arg Pro Arg Glu Arg Asn His Leu Pro
195 200 205

Glu Asp Thr Glu Pro Gly Leu Gly Glu Ser Gln Leu Glu Thr Gly Ser
210 215 220

Phe Leu Asp His Ala Ala Pro Leu Thr Leu Pro Pro Gly Trp Arg Gln
 225 230 235 240

Arg Gln Pro Pro Thr Pro Ala Pro Asp Pro Pro Pro Ile Pro Leu Cys Thr
245 250 255

Lys Ser Leu Ser Ser Gly Asn Cys Ile
260 265

<210> 50

<211> 795

<212> DNA

<213> *Felis catus*

<400> 50

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cgttqqqqqc tqgcgttqcc tccatccccq qqqqqaqaqtq aqcqqqqqcaq cqtqatcqaq 120

gaagggaaacca qtctctaqt qactttctcc qaqtcccqqc tctatqtctt cqqqcaqqta 180

attcctctct ctgggcctca gtgtcttcct ctgctccctg gggtagggcg ttctccatct 240
ccttcttcgc cagtgcaggc accaggcggc ggacatcagc aagagagcca caggcaacag 300
cagcaggagg agcagcagag gggcctgagg ggctggcagg gctgtggcct ccaaggccct 360
ggggctcctt gggggcagtg gggtgagga gtcgggctga cactgtagct ccaggcaccc 420
cgagaaattc ctgcgggtga tccagggctt caaggccgcc agctgctcgg aggtgtcctg 480
caggaggtgg gagatgttgg tctggacgaa tcgaagacag ctggggaggg gctggaaggc 540
acacaaggtg acaaaatgta tctcggttt gaccgcctcc agcaggctt gcatctggga 600
cccagccaca gccttgagcc gacccatcca gcgctggcc aggaccaggt gccagaatgg 660
cccacagagc tcgtcgtcct gtaggttgg ggcgacggtg actggtaat cctgaagcag 720
gtaatcagac agcttcgga tggtgacctt gaaggtggag gagatggggc tgtggctgaa 780
ggaacagtcg gggga 795

<210> 51
<211> 321
<212> DNA
<213> *Canis familiaris*

<400> 51
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gtgaaggttc aggccggAAC taacaagact gatgttatct gtggtccccca gcctcggtta 120
agagccctag tggtggtccc catcattatg gggatcctgc ttgttgctt gttgggtct 180
gcctgcattcc gaaagggtgg caagaagcca gagaataagg ttatgtatca ggaccctgtg 240
gaggacttgg aggaatttcc tatgcccccg cactccattt ctccggtgca agagacctta 300
catgggtgcc agcccgatcac c 321

<210> 52
<211> 1425
<212> DNA
<213> *Canis familiaris*

<220>

<221> CDS

<222> (196)...(1017)

<400> 52

tagactcccg ggaatattca ggggaactcc cggcgctaag ggtctccagg agctccgccc 60

tgcccaacga agccggccac gattggtccc cgaagacccc gcccatctcc tggcggggc 120

ggcgggggc aaggctggg gagttactaa agacatcccc gcgcctac tccgctgcct 180

gctattcacc tcgcc atg gtt ctc ctg cct ctg cgc tgt ctc ttc tgg ggc 231
Met Val Leu Leu Pro Leu Arg Cys Leu Phe Trp Gly

1

5

10

tcc ttg ttg acc acc gtc tac cca gaa cca cgc act gca tgc aga gaa 279
Ser Leu Leu Thr Thr Val Tyr Pro Glu Pro Arg Thr Ala Cys Arg Glu

15

20

25

aag caa tac cta gta gac agt cag tgc tgt aat atg tgc cca cca gga 327
Lys Gln Tyr Leu Val Asp Ser Gln Cys Cys Asn Met Cys Pro Pro Gly

30

35

40

gag aaa ctg gtg aat gac tgc cta cat acc att gac acg gaa tgc act 375
Glu Lys Leu Val Asn Asp Cys Leu His Thr Ile Asp Thr Glu Cys Thr

45

50

55

60

cgt tgc caa aca ggc gaa ttc cta gac act tgg aac gca gag aga cac 423
Arg Cys Gln Thr Gly Glu Phe Leu Asp Thr Trp Asn Ala Glu Arg His

65

70

75

tgt cac cag cac aaa tac tgc gac ccc aac cta ggg ctc cat gtc gag 471
Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly Leu His Val Glu

80

85

90

aag gag ggc acg tca gaa aca gac acc act tgc aca tgc gat gaa ggt 519
Lys Glu Gly Thr Ser Glu Thr Asp Thr Cys Thr Cys Asp Glu Gly

95

100

105

ctg cat tgt acc aac gct gcc tgt gag agc tgc acc atg cac agc ctg 567
Leu His Cys Thr Asn Ala Ala Cys Glu Ser Cys Thr Met His Ser Leu

110

115

120

tgc ccc cct ggc ctg gga gtc aaa cag atc gct aca ggg att tct gat 615
Cys Pro Pro Gly Leu Gly Val Lys Gln Ile Ala Thr Gly Ile Ser Asp

125

130

135

140

acc atc tgc gat ccc tgc ccc atc ggc ttc ttc tcc aat gtg tct tct 663
Thr Ile Cys Asp Pro Cys Pro Ile Gly Phe Phe Ser Asn Val Ser Ser

145 150 155

gct ttg gaa aag tgt cac cct tgg aca agc tgt gaa acc aaa ggc ctg 711
Ala Leu Glu Lys Cys His Pro Trp Thr Ser Cys Glu Thr Lys Gly Leu
160 165 170

gtg aag gtt cag gcg gga act aac aag act gat gtt atc tgt ggt ccc 759
Val Lys Val Gln Ala Gly Thr Asn Lys Thr Asp Val Ile Cys Gly Pro
175 180 185

cag cct cgg tta aga gcc cta gtg gtg gtc ccc atc att atg ggg atc 807
Gln Pro Arg Leu Arg Ala Leu Val Val Val Pro Ile Ile Met Gly Ile
190 195 200

ctg ctt gtt gtc ctg ttg gtg tot gcc tgc atc cga aag gtg gtc aag 855
Leu Leu Val Val Leu Val Ser Ala Cys Ile Arg Lys Val Val Lys
205 210 215 220

aag cca gag aat aag gtt atg tat cag gac cct gtg gag gac ttg gag 903
Lys Pro Glu Asn Lys Val Met Tyr Gln Asp Pro Val Glu Asp Leu Glu
225 230 235

gaa ttt cct atg ccc ccg cac tcc att gct ccg gtg caa gag acc tta 951
Glu Phe Pro Met Pro Pro His Ser Ile Ala Pro Val Gln Glu Thr Leu
240 245 250

cat ggg tgc cag ccc gtc acc cag gag gac ggc aaa gag agc cgc atc 999
His Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile
255 260 265

tcc gtg cag gag aga gtg tgaggcagcg tggccagg agtgtgacag 1047
Ser Val Gln Glu Arg Val
270

cgtggagag tggcgcggtg gctggagagc ctggagctgc tggagggca tgaagggcg 1107

gtgctccct gcctgcaccc ctgtgctgca gaaacagaga accttccacc ccacccctgg 1167

agcccattcc acctccaaac ttgctttaa agatggagat gaaactttg gggggccaga 1227

tagtaatatc caccaaccca gcatttcagg gccctgaggt gtatatcacg gtggttcta 1287

cgagcccagg aagacccacg aagagccatt gtggcattgt ttgtgacagt ggacaactgg 1347

aggccactta gctgttcagc agcaggggac tggctaaata aaattttaa tatattata 1407

aaaaaaaaaaaa aaaaaaaaaa 1425

<210> 53

<211> 274

<212> PRT

<213> Canis familiaris

<400> 53

Met Val Leu Leu Pro Leu Arg Cys Leu Phe Trp Gly Ser Leu Leu Thr
1 5 10 15

Thr Val Tyr Pro Glu Pro Arg Thr Ala Cys Arg Glu Lys Gln Tyr Leu
20 25 30

Val Asp Ser Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val
35 40 45

Asn Asp Cys Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr
50 55 60

Gly Glu Phe Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His
65 70 75 80

Lys Tyr Cys Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr
85 90 95

Ser Glu Thr Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr
100 105 110

Asn Ala Ala Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly
115 120 125

Leu Gly Val Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp
130 135 140

Pro Cys Pro Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys
145 150 155 160

Cys His Pro Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln
165 170 175

Ala Gly Thr Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu
180 185 190

Arg Ala Leu Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val
195 200 205

Leu Leu Val Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn
210 215 220

Lys Val Met Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met
225 230 235 240

Pro Pro His Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln
245 250 255

Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu
260 265 270

Arg Val

<210> 54

<211> 1425

<212> DNA

<213> Canis familiaris

<400> 54

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tgggtcttcc tgggctcgta gaaaccaccc tgatatacac ctcagggccc taaaatgctg 180

ggttggtgga tattactatc tggccccc aagtttcat ctccatctt aaaagcaagt 240

tgggaggtgg aatgggctcc aggggtgggg tggaaggttc tctgtttctg cagcacaggg 300

gtgcaggcag gggagcaccc ccccttcatg cccctccagc agctccaggg tctccagcca 360

cgcgcccact ctcccacgct gtcacactcc tggcacacgg ctgcctcaca ctctctcctg 420

cacggagatg cggctctctt tgccgtcctc ctgggtgacg ggctggcacc catgtaaagg 480

ctcttgaccc ggagcaatgg agtgcggggg cataggaaat tcctccaagt cctccacagg 540

gtcctgatac ataaccttat tctctggctt cttgaccacc ttccggatgc aggcagacac 600

caacaggaca acaagcagga tccccataat gatggggacc accactaggg ctcttaaccg 660

aggctggggg ccacagataa catcagtctt gttagttccc gcctgaacct tcaccaggcc 720

tttggtttca cagctgtcc aagggtgaca ctttccaaa gcagaagaca cattggagaa 780

gaagccgatg gggcagggat cgccagatggt atcagaaatc cctgtagcga tctgtttgac 840

tcccaggcca gggggcaca ggctgtgcat ggtgcagctc tcacaggcag cgttggtaca 900
atgcagacacct tcatcgcatg tgcaagtggt gtctgttct gacgtgcctt ccttctcgac 960
atggagccct aggtgggggt cgcaagtattt gtgtgggtga cagtgtctct ctgcgttcca 1020
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gtcattcacc agtttctctc ctgggtggca catattacag cactgactgt ctactaggtta 1140
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gaagagacag cgcaaggca ggagaaccat ggcaagggtga atagcaggca gcggagtagg 1260
ggcgccggga tgtcttttagt aactccccag cccttgcccc cgcccgcccc gcccaggaga 1320
tggcgccgggt cttcgccggac caatcggtgc cggcttcgtt gggcaggcgag gagctcctgg 1380
agacccttag cgccgggagt tcccctgaat attcccgggaa gtcta 1425

<210> 55
<211> 822
<212> DNA
<213> Canis familiaris

<400> 55
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gaaccacgca ctgcattgcag agaaaagcaa taccttagtag acagtcagtg ctgtaatatg 120
tgcccaccag gagagaaact ggtgaatgac tgcctacata ccattgacac ggaatgcact 180
cgttgccaaa caggcgaatt cctagacact tggAACGcag agagacactg tcaccagcac 240
aaatactgctg accccaacccctt agggctccat gtcgagaagg agggcacgtc agaaacagac 300
accacttgca catgcgtatga aggtctgcat tgtaccaacg ctgcctgtga gagctgcacc 360
atgcacagcc tggccccc tggcctggaa gtcaaacaga tcgctacagg gatttctgat 420
accatctgctg atccctgcccc catcggttc ttctccaaatg tgtcttgc tttggaaaag 480
tgtcaccctt ggacaagctg tgaaacccaa ggcctgggtga aggttcaggc gggaaactaac 540
aagactgatg ttatctgtgg tccccagcctt cggtaagag ccctagtggt ggtccccatc 600
attatggggaa tcctgcttgc tggcctgttgc gtgtctgcctt gcatccgaaa ggtggtaag 660

aagccagaga ataaggatgtatcaggac cctgtggagg acttggagga atttcctatg 720
cccccgact ccattgctcc ggtgcaagag accttacatg ggtgccagcc cgtcacccag 780
gaggacggca aagagagccg catctccgtg caggagagag tg 822

<210> 56
<211> 822
<212> DNA
<213> Canis familiaris

<400> 56
cactctctcc tgcacggaga tgccggcttc tttgccgtcc tcctgggtga cgggctggca 60
cccatgtaaag gtctcttgca ccggagcaat ggagtgcggg ggcataggaa attcctccaa 120
gtcctccaca gggtcctgat acataaccctt attctctggc ttcttgacca ccttcggat 180
gcaggcagac accaacacagga caacaaggcag gatccccata atgatgggga ccaccactag 240
ggctcttaac cgaggctggg gaccacagat aacatcagtc ttgttagttc ccgcctgaac 300
cttcaccagg ccttgggtt cacagctgt ccaagggtga cactttcca aagcagaaga 360
cacattggag aagaagccga tggggcaggg atcgcagatg gtatcagaaa tccctgttagc 420
gatctgtttg actcccaggc caggggggca caggctgtgc atggtgacgc tctcacagggc 480
agcgttggta caatgcagac cttcatcgca tgtcaagtg gtgtctgttt ctgacgtgcc 540
ctccttctcg acatggagcc ctaggttggg gtcgcagtat ttgtgctggc gacagtgtct 600
ctctgcgttc caagtgtcta ggaattcgcc tgttggcaa cgagtgcatt ccgtgtcaat 660
ggtatgtagg cagtcattca ccagttctc tcctgggtgg cacatattac agcactgact 720
gtctactagg tattgtttt ctctgcgtgc agtgcgtgg tctggtaga cggtggtcaa 780
caaggagccc cagaagagac agcgcagagg caggagaacc at 822

<210> 57
<211> 765
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(765)

<400> 57

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Pro	Glu	Pro	Arg	Thr	Ala	Cys	Arg	Glu	Lys	Gln	Tyr	Leu	Val	Asp	Ser	
1		5						10						15		

cag tgc tgt aat atg tgc cca cca gga gag aaa ctg gtg aat gac tgc 96
Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val Asn Asp Cys
20 25 30

cta cat acc att gac acg gaa tgc act cgt tgc caa aca ggc gaa ttc 144
Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr Gly Glu Phe
35 40 45

cta gac act tgg aac gca gag aga cac tgt cac cag cac aaa tac tgc 192
Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His Lys Tyr Cys
50 55 60

gac ccc aac cta ggg ctc cat gtc gag aag gag ggc acg tca gaa aca 240
Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr Ser Glu Thr
65 70 75 80

gac acc act tgc aca tgc gat gaa ggt ctg cat tgt acc aac gct gcc 288
Asp Thr Thr Cys Thr Asp Glu Gly Leu His Cys Thr Asn Ala Ala
85 90 95

tgt gag agc tgc acc atg cac agc ctg tgc ccc cct ggc ctg gga gtc 336
Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly Leu Gly Val
100 105 110

aaa cag atc gct aca ggg att tct gat acc atc tgc gat ccc tgc ccc 384
Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp Pro Cys Pro
115 120 125

atc ggc ttc ttc tcc aat gtg tct tct gct ttg gaa aag tgt cac cct 432
Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys Cys His Pro
130 135 140

tgg aca agc tgt gaa acc aaa ggc ctg gtg aag gtt cag gcg gga act 480
Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln Ala Gly Thr
145 150 155 160

aac aag act gat gtt atc tgt ggt ccc cag cct cggttta aga gcc cta 528
Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu Arg Ala Leu
165 170 175

gtg gtg gtc ccc atc att atg ggg atc ctg ctt gtt gtc ctg ttg gtg 576
Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val Leu Leu Val
180 185 190

tct gcc tgc atc cga aag gtg gtc aag aag cca gag aat aag gtt atg 624
Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn Lys Val Met
195 200 205

tat cag gac cct gtg gag gac ttg gag gaa ttt cct atg ccc ccg cac 672
Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met Pro Pro His
210 215 220

tcc att gct ccg gtg caa gag acc tta cat ggg tgc cag ccc gtc acc 720
Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr
225 230 235 240

cag gag gac ggc aaa gag agc cgc atc tcc gtg cag gag aga gtg 765
Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu Arg Val
245 250 255

<210> 58
<211> 255
<212> PRT
<213> Canis familiaris

<400> 58
Pro Glu Pro Arg Thr Ala Cys Arg Glu Lys Gln Tyr Leu Val Asp Ser
1 5 10 15
Gln Cys Cys Asn Met Cys Pro Pro Gly Glu Lys Leu Val Asn Asp Cys
20 25 30

Leu His Thr Ile Asp Thr Glu Cys Thr Arg Cys Gln Thr Gly Glu Phe
35 40 45

Leu Asp Thr Trp Asn Ala Glu Arg His Cys His Gln His Lys Tyr Cys
50 55 60

Asp Pro Asn Leu Gly Leu His Val Glu Lys Glu Gly Thr Ser Glu Thr
65 70 75 80

Asp Thr Thr Cys Thr Cys Asp Glu Gly Leu His Cys Thr Asn Ala Ala
85 90 95

Cys Glu Ser Cys Thr Met His Ser Leu Cys Pro Pro Gly Leu Gly Val
100 105 110

Lys Gln Ile Ala Thr Gly Ile Ser Asp Thr Ile Cys Asp Pro Cys Pro
115 120 125

Ile Gly Phe Phe Ser Asn Val Ser Ser Ala Leu Glu Lys Cys His Pro
130 135 140

Trp Thr Ser Cys Glu Thr Lys Gly Leu Val Lys Val Gln Ala Gly Thr
145 150 155 160

Asn Lys Thr Asp Val Ile Cys Gly Pro Gln Pro Arg Leu Arg Ala Leu
165 170 175

Val Val Val Pro Ile Ile Met Gly Ile Leu Leu Val Val Leu Leu Val
180 185 190

Ser Ala Cys Ile Arg Lys Val Val Lys Lys Pro Glu Asn Lys Val Met
195 200 205

Tyr Gln Asp Pro Val Glu Asp Leu Glu Glu Phe Pro Met Pro Pro His
210 215 220

Ser Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr
225 230 235 240

Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser Val Gln Glu Arg Val
245 250 255

<210> 59

<211> 765

<212> DNA

<213> Canis familiaris

<400> 59

cactctctcc tgcacggaga tgcggctctc tttgccgtcc tcctgggtga cgggctggca 60

cccatgtaaag gtctcttgca ccggagcaat ggagtgcggg ggcataggaa attcctccaa 120

gtcctccaca gggcctgtat acataaccctt attctctggc ttcttgacca ccttcggat 180

gcaggcagac accaacagga caacaagcag gatccccata atgatgggaa ccaccactag 240

ggctcttaac cgaggctggg gaccacagat aacatcagtc ttgttagttc ccgcctgaac 300

cttcaccagg ccttgggtt cacagctgt ccaagggtga cactttcca aagcagaaga 360

cacattggag aagaagccga tggggcaggg atcgcagatg gtatcagaaa tccctgtac 420

gatctgtttg actcccaggc caggggggca caggctgtgc atggtgacgc tctcacaggc 480
agcggtggta caatgcagac cttcatcgca tgtgcaagtg gtgtctgttt ctgacgtgcc 540
ctccttctcg acatggagcc ctagggtggg gtcgcagtat ttgtgctggc gacagtgtct 600
ctctgcgttc caagtgtcta ggaattcgcc tggtggcaa cgagtgcatt ccgtgtcaat 660
ggtatgttagg cagtcattca ccagttctc tcctgggtgg cacatattac agcaactgact 720
gtctactagg tattgctttt ctctgcatgc agtgcgtggc tctgg 765

<210> 60
<211> 336
<212> DNA
<213> *Felis catus*

<220>
<221> CDS
<222> (1)..(336)

<400> 60
aat gtg tca tct gct tcg gaa aag tgt cac cct tgg acg agg tgt gag 48
Asn Val Ser Ser Ala Ser Glu Lys Cys His Pro Trp Thr Arg Cys Glu
1 5 10 15

acc aaa ggc ctg gtg gag ctt cag gcg ggg acc aac aag acg gat gcc 96
Thr Lys Gly Leu Val Glu Leu Gln Ala Gly Thr Asn Lys Thr Asp Ala
20 25 30

gtc tgc ggt ttc cag gat cgg ata aga gcc ctg gtg gtg atc ccc atc 144
Val Cys Gly Phe Gln Asp Arg Ile Arg Ala Leu Val Val Ile Pro Ile
35 40 45

acg atg gtg gtc ctg ctt gct gtc ttg ttg gtg tct gcg tat atc aga 192
Thr Met Val Val Leu Leu Ala Val Leu Leu Val Ser Ala Tyr Ile Arg
50 55 60

aag gtg acc aag aag cca gag aat aag gtc ctc cag cct aag gct gtg 240
Lys Val Thr Lys Lys Pro Glu Asn Lys Val Leu Gln Pro Lys Ala Val
65 70 75 80

tcg cag gac cct gtg gag gac ttg gag gtc ctt cct gtc ccc ctc cac 288
Ser Gln Asp Pro Val Glu Asp Leu Glu Val Leu Pro Val Pro Leu His
85 90 95

ccc att gct ccg gtg cag gag acc tta cac ggg tgc cag ccg gtc acc 336
Pro Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr
100 105 110

<210> 61
<211> 112
<212> PRT
<213> Felis catus

<400> 61
Asn Val Ser Ser Ala Ser Glu Lys Cys His Pro Trp Thr Arg Cys Glu
1 5 10 15

Thr Lys Gly Leu Val Glu Leu Gln Ala Gly Thr Asn Lys Thr Asp Ala
20 25 30

Val Cys Gly Phe Gln Asp Arg Ile Arg Ala Leu Val Val Ile Pro Ile
35 40 45

Thr Met Val Val Leu Leu Ala Val Leu Leu Val Ser Ala Tyr Ile Arg
50 55 60

Lys Val Thr Lys Lys Pro Glu Asn Lys Val Leu Gln Pro Lys Ala Val
65 70 75 80

Ser Gln Asp Pro Val Glu Asp Leu Glu Val Leu Pro Val Pro Leu His
85 90 95

Pro Ile Ala Pro Val Gln Glu Thr Leu His Gly Cys Gln Pro Val Thr
100 105 110

<210> 62
<211> 336
<212> DNA
<213> Felis catus

<400> 62
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aggaaggacc tccaaagtccct ccacagggtc ctgcgcacaca gccttaggct ggaggacctt 120
attctctggc ttcttggtca cctttctgat atacgcagac accaacaaga cagcaagcag 180
gaccaccatc gtgatgggga tcaccaccag ggctcttatac cgatcctgga aaccgcagac 240
ggcatccgtc ttgttggtcc cccgctgaag ctccaccagg cctttggtct cacacctcgt 300

ccaagggtga cactttccg aagcagatga cacatt

336

<210> 63

<211> 390

<212> DNA

<213> Canis familiaris

<400> 63

ataaagtgagg ctagtagtaa cccagcgtcc gttctgcgg gggcgccaaa agggtaactac 60

accataagca gcaacctggt gagcctcgag aatggaaac agttggccgt gaaaagacaa 120

ggactctatt acgtctatgc ccaagtcacc ttctgctcca atcgggcagc ttcgagtcaa 180

gtcccgttcg tcgccagcct atgcctccat tccccgagtg gaacggagag agtcttactc 240

cgcgcgcga gctccgcgg ctcgtccaaa cttgcggcc aacagtccat ccacttggga 300

ggagtatttg aattgcatcc aggtgcttcg gtgttcgtca acgtgactga tccaagccaa 360

gtgagccacg ggaccggctt cacgtctttt 390

<210> 64

<211> 1878

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (284)..(1063)

<400> 64

aatgtatgga agaagaaaact tggttcttct ttactaacaa aagggaaagc ctgaaagtga 60

atgatatggg tataattaaa aaaaaaaaaa aaaaaaaaaa aaaaccttta cgtaactttt 120

tttgctggga gagaagacta cgaagcacat tttccagaa gtgtggctg caacgattgt 180

gcgcctttaa ctaatcctga gtaaggtggc cacttgaca gtgtttcat gctgcctctg 240

ccaccttctc ggtctgaaga tatcatttca actctaacac agc atg atc gaa aca 295

Met Ile Glu Thr

1

tat agc caa act gct ccc cga tct gtg gcc act gga cca ccc gtc agt 343

Tyr	Ser	Gln	Thr	Ala	Pro	Arg	Ser	Val	Ala	Thr	Gly	Pro	Pro	Val	Ser	
5				10					15					20		
atg aaa att ttt atg tat ttg ctt act gtt ttt ctc atc acc cag atg															391	
Met	Lys	Ile	Phe	Met	Tyr	Leu	Leu	Thr	Val	Phe	Leu	Ile	Thr	Gln	Met	
				25				30				35				
att gga tcg gca ctc ttt gct gta tat ctt cac aga aga ttg gac aag															439	
Ile	Gly	Ser	Ala	Leu	Phe	Ala	Val	Tyr	Leu	His	Arg	Arg	Leu	Asp	Lys	
				40			45			50						
ata gaa gat gaa agg aat ctt tat gaa gat ttt gtg ttc atg aaa acg															487	
Ile	Glu	Asp	Glu	Arg	Asn	Leu	Tyr	Glu	Asp	Phe	Val	Phe	Met	Lys	Thr	
				55			60			65						
tta cag aaa tgc aac aaa ggg gag ggg tcc ttg tcc tta ctg aac tgt															535	
Leu	Gln	Lys	Cys	Asn	Lys	Gly	Glu	Gly	Ser	Leu	Ser	Leu	Leu	Asn	Cys	
				70			75			80						
gag gaa att aaa agc caa ttt gaa gcc ttt ctc aag gag ata atg cta															583	
Glu	Glu	Ile	Lys	Ser	Gln	Phe	Glu	Ala	Phe	Leu	Lys	Glu	Ile	Met	Leu	
				85			90			95			100			
aac aac gaa atg aag aaa gaa aac att gca atg caa aaa ggt gat															631	
Asn	Asn	Glu	Met	Lys	Glu	Glu	Asn	Ile	Ala	Met	Gln	Lys	Gly	Asp		
				105			110			115						
cag gat cct cga att gca gcc cat gtc ata agt gag gct agt agt aac															679	
Gln	Asp	Pro	Arg	Ile	Ala	Ala	His	Val	Ile	Ser	Glu	Ala	Ser	Ser	Asn	
				120			125			130						
cca gcg tcc gtt ctg cgg tgg gcg cca aaa ggg tac tac acc ata agc															727	
Pro	Ala	Ser	Val	Leu	Arg	Trp	Ala	Pro	Lys	Gly	Tyr	Tyr	Thr	Ile	Ser	
				135			140			145						
agc aac ctg gtg agc ctc gag aat ggg aaa cag ttg gcc gtg aaa aga															775	
Ser	Asn	Leu	Val	Ser	Leu	Glu	Asn	Gly	Lys	Gln	Leu	Ala	Val	Lys	Arg	
				150			155			160						
caa gga ctc tat tac gtc tat gcc caa gtc acc ttc tgc tcc aat cgg															823	
Gln	Gly	Leu	Tyr	Tyr	Val	Tyr	Ala	Gln	Val	Thr	Phe	Cys	Ser	Asn	Arg	
				165			170			175			180			
gca gct tcg agt caa gct ccg ttc gtc gcc agc cta tgc ctc cat tcc															871	
Ala	Ala	Ser	Ser	Gln	Ala	Pro	Phe	Val	Ala	Ser	Leu	Cys	Leu	His	Ser	
				185			190			195						
ccg agt gga acg gag aga gtc tta ctc cgc gcc gcg agc tcc cgc ggc															919	

Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser Ser Arg Gly		
200	205	210
tcg tcc aaa cct tgc ggc caa cag tcc atc cac ttg gga gga gta ttt	967	
Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe		
215	220	225
gaa ttg cat cca ggt gct tcg gtg ttc gtc aac gtg act gat cca agc	1015	
Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser		
230	235	240
caa gtg agc cac ggg acc ggc ttc acg tct ttt ggc tta ctc aaa ctc	1063	
Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu		
245	250	260
tgagtgctgg cacctcacag gctgcagctc agctcctgtt ggtggcttc gtaatacggc	1123	
cgagcagtttta agaccaccac ccctgttcaa ctgcctattt ataacccttag gatcctcctc	1183	
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cactgatgca gacatccaga gagtccatg aaaaagacga gactattatg cacagattga	1363	
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tttcactgga gaatgtactc gatttccccg cgaagatgct gaaggcaac agggagcctc	1483	
agtcacagt cagttacggt tgacccgggg tccccgggc cccgatggag gggacaggct	1543	
ccagaaagtc tcatggcgcg gagaactgga aaaccctgcc cccaccagcc accctgacac	1603	
tcattctctc cctcctccgc ccccccccccc ccacagtcag gctgttgcta atcggttata	1663	
ttatttcaac cctgttgctt ctccaccagt gttagcggga ggagagagca gaggctgccc	1723	
actcctcctc ctgaaatgac ttttttttttggaaatctt cctacctacc tgcagtctcc	1783	
attgtttcca gagtgaactt gtgattatct tttttttttttaataaagcgcc	1843	
cttaacgtta aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaa	1878	

<210> 65
 <211> 260
 <212> PRT
 <213> Canis familiaris

<400> 65

Met Ile Glu Thr Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Thr Gly
1 5 10 15

Pro Pro Val Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
20 25 30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg
35 40 45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val
50 55 60

Phe Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser
65 70 75 80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys
85 90 95

Glu Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met
100 105 110

Gln Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu
115 120 125

Ala Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr
130 135 140

Tyr Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu
145 150 155 160

Ala Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe
165 170 175

Cys Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu
180 185 190

Cys Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala
195 200 205

Ser Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu
210 215 220

Gly Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val
225 230 235 240

Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly

245

250

255

Leu Leu Lys Leu
260

<210> 66
<211> 1878
<212> DNA
<213> Canis familiaris

<400> 66
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taacaagata atcacaagtt cactctggaa acaatggaga ctgcaggtag gtaggagaga 120
tttcctttaa atacagtcat ttcaggagga ggagtggca gcctctgctc tctcctccg 180
cctacactgg tggagaggca acagggttga aataagataa ccgattagca acagcctgac 240
tgtgggggga ggggggcgga ggagggagag aatgagtgtc agggtggctg gtggggcag 300
ggttttccag ttctccgcgc catcagactt tctggagcct gtcccctcca tcggggcccc 360
ggggaccccg ggtcaaccgt aactgactgt gagctgaggc tccctgttgc ctttcagcat 420
cttcgcgggg aaatcgagta cattctccag taaaagacac tgcatac 480
gaaactggac taattatctg ccgtttactg aggattcaat ctgtgcataa tagtctcg 540
tttttcatgg gactctctgg atgtctgcat cagtggggcg gctgcttcca gaatatcaac 600
tcttaccgac cggggcctgt tggcgctgcc cccgcccgt cattcccttc ttgcagccct 660
ccacgcctgg gggtgtataa taaatagttc tccacgagga ggatcctagg gttataaata 720
ggcagttcaa caggggtgg ggtcttaact gctcggccgt attacgaaga ccaccaacag 780
gagctgagct gcagcctgtg aggtgccagc actcagagtt tgagtaagcc aaaagacgtg 840
aagccggtcc cgtggctcac ttggcttggc tcagtcacgt tgacgaacac cgaagcacct 900
ggatgcaatt caaatactcc tcccaagtgg atggactgtt ggccgcaagg tttggacgag 960
ccgcgggagc tcgcggcgcg gagtaagact ctctccgttc cactcgggaa atggaggcat 1020
aggctggcga cgaacggagc ttgactcgaa gctgcccgt tggagcagaa ggtgacttgg 1080

gcatagacgt aatagagtc ttgtctttc acggccaact gtttccatt ctgcaggctc 1140
accaggttgc tgcttatggt gtagtaccct tttggcgccc accgcagaac ggacgctggg 1200
ttactactag cctcacttat gacatggct gcaattcgag gatcctgatc accttttgc 1260
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catttctgtt acgttttcat gaacacaaaa tcttcataaa gattccttgc atcttctatc 1440
ttgtccaatc ttctgtgaag atatacagca aagagtgcgg atccaatcat ctgggtgatg 1500
agaaaaacag taagcaaata cataaaaatt ttcatactga cgggtggtcc agtggccaca 1560
gatcggggag cagtttgct atatgttgc atcatgctgt gtttaggtt aatgtatc 1620
ttcagaccga gaagggtggca gaggcagcat gaaaacactg tcaaagtggc caccttactc 1680
aggattagtt aagagcgcac aatcggttgc gcccacactt cctggaaaat gtgcttcgta 1740
gtcttctctc ccagcaaaaa aagttacgta aaggttttt ttttttttt ttttttttt 1800
taattataacc catatcattt acttccaggc tttccctttt gtttagtaaag aagaaacaag 1860
tttcttcttc catacatt 1878

<210> 67
<211> 780
<212> DNA
<213> *Canis familiaris*

<400> 67
atgatcgaaa catatagcca aactgctccc cgatctgtgg ccactggacc acccgtagt 60
atgaaaattt ttatgtattt gcttactgtt tttctcatca cccagatgat tggatcggca 120
ctctttgctg tatactttca cagaagattt gacaagatag aagatgaaag gaatctttat 180
gaagattttt tgttcatgaa aacgttacag aaatgcaaca aaggggaggg gtccttgc 240
ttactgaact gtgaggaaat taaaagccaa tttgaaggct ttctcaagga gataatgcta 300
aacaacgaaa tgaagaaaga agaaaaacatt gcaatgcaaa aaggtgatca ggatcctcga 360
attgcagccc atgtcataag tgaggctagt agtaacccag cgtccgttct gcgggtggcg 420

ccaaaagggt actacaccat aagcagcaac ctggtgagcc tcgagaatgg gaaacagttg 480
gccgtaaaa gacaaggact ctattacgtc tatgcccaag tcacccttctg ctccaatcgg 540
gcagcttcga gtcaagctcc gttcgtcgcc agcctatgcc tccattcccc gagtggaaacg 600
gagagagtct tactccgcgc cgcgagctcc cgcggtcggt ccaaacccttg cggccaacag 660
tccatccact tgggaggagt atttgaattt catccaggtt ctccgggttt cgtcaacgtt 720
actqatccaa qccaagtqaq ccacqqqacc qqcttcacgt cttttqgctt actcaaactc 780

<210> 68
<211> 780
<212> DNA
<213> *Canis familiaris*

<400> 68
gagttttagt aagccaaaag acgtgaagcc ggtcccgtagt ctcacttggc ttggatcagt 60
cacgtttagt aacaccgaaag cacctggatg caattcaaat actcctccca agtggatgga 120
ctgttggccg caagggttgg acgagccgatg ggagctcgatg gcgccggagta agactctc 180
cgttccactc gggaaatgga ggcataaggct ggcgacgaaac ggagcttgc tcgaagctgc 240
ccgattggag cagaagggtga cttgggcata gacgtaatag agtccttgc ttacacggc 300
caactgtttc ccattctcgat ggctcaccatg gttgctgctt atggtgttagt accctttgg 360
cgccccaccgc agaacggacg ctgggttact actagcctca cttatgacat gggctgcaat 420
tcgaggatcc tgatcacctt tttgcattgc aatgtttct tctttcttca ttgcgttgg 480
tagcattatc tccttgagaa aggctcaaa ttggctttta atttcctcac agttcagtaa 540
ggacaaggac ccctccctt tggtgcattt ctgtAACGTT ttcatgaaca caaaatcttc 600
ataaaagattc ctgcattttt ctatcttgc caatcttctg tgaagatata cagcaaagag 660
tgccgatcca atcatctggg tggatgagaaa aacagtaagc aaatacataa aaattttcat 720
actgacqqqt qgtccaaqtqq ccacaaqatcq qqqaqcqattt tggatataatq ttgcgtatcat 780

<210> 69

<211> 633

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(633)

<400> 69

ttg gac aag ata gaa gat gaa agg aat ctt tat gaa gat ttt gtg ttc 48
Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
1 5 10 15

atg aaa acg tta cag aaa tgc aac aaa ggg gag ggg tcc ttg tcc tta 96
Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu
20 25 30

ctg aac tgt gag gaa att aaa agc caa ttt gaa gcc ttt ctc aag gag 144
Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu
35 40 45

ata atg cta aac aac gaa atg aag aaa gaa gaa aac att gca atg caa 192
Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln
50 55 60

aaa ggt gat cag gat cct cga att gca gcc cat gtc ata agt gag gct 240
Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala
65 70 75 80

agt agt aac cca gcg tcc gtt ctg cgg tgg gcg cca aaa ggg tac tac 288
Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr
85 90 95

acc ata agc agc aac ctg gtg agc ctc gag aat ggg aaa cag ttg gcc 336
Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala
100 105 110

gtg aaa aga caa gga ctc tat tac gtc tat gcc caa gtc acc ttc tgc 384
Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys
115 120 125

tcc aat cgg gca gct tcg agt caa gct ccg ttc gtc gcc agc cta tgc 432
Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys
130 135 140

ctc cat tcc ccg agt gga acg gag aga gtc tta ctc cgc gcc gcg agc 480
Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser
145 150 155 160

tcc cgc ggc tcg tcc aaa cct tgc ggc caa cag tcc atc cac ttg gga 528
Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
165 170 175

gga gta ttt gaa ttg cat cca ggt gct tcg gtg ttc gtc aac gtg act 576
Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr
180 185 190

gat cca agc caa gtg agc cac ggg acc ggc ttc acg tct ttt ggc tta 624
Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
195 200 205

ctc aaa ctc 633
Leu Lys Leu
210

<210> 70
<211> 211
<212> PRT
<213> Canis familiaris

<400> 70
Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
1 5 10 15

Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu
20 25 30

Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Ala Phe Leu Lys Glu
35 40 45

Ile Met Leu Asn Asn Glu Met Lys Lys Glu Glu Asn Ile Ala Met Gln
50 55 60

Lys Gly Asp Gln Asp Pro Arg Ile Ala Ala His Val Ile Ser Glu Ala
65 70 75 80

Ser Ser Asn Pro Ala Ser Val Leu Arg Trp Ala Pro Lys Gly Tyr Tyr
85 90 95

Thr Ile Ser Ser Asn Leu Val Ser Leu Glu Asn Gly Lys Gln Leu Ala
100 105 110

Val Lys Arg Gln Gly Leu Tyr Tyr Val Tyr Ala Gln Val Thr Phe Cys
115 120 125

Ser Asn Arg Ala Ala Ser Ser Gln Ala Pro Phe Val Ala Ser Leu Cys
130 135 140

Leu His Ser Pro Ser Gly Thr Glu Arg Val Leu Leu Arg Ala Ala Ser
145 150 155 160

Ser Arg Gly Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
165 170 175

Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr
180 185 190

Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
195 200 205

Leu Lys Leu
210

<210> 71

<211> 633

<212> DNA

<213> Canis familiaris

<400> 71

gagtttgagt aagccaaaag acgtgaagcc ggtcccgtagt ctcacttggc ttggatcagt 60

cacgttgacg aacaccgaag cacctggatg caattcaaat actcctccca agtggatgga 120

ctgttggccg caagggttgg acgagccgacg ggagctcgac ggcggagta agactctc 180

cgttccactc gggaaatgga ggcatacgatc ggagcttgc ac tcaagctgc 240

ccgattggag cagaaggta cttggcata gacgtaatag agtccttgc tttcacggc 300

caactgttc ccattctcga ggctcaccag gttgctgctt atgggttagt accctttgg 360

cggccaccgc agaacggacg ctgggttact actagcctca cttatgacat gggctgcaat 420

tcgaggatcc tgcacacctt ttgcattgc aatgtttct tctttctca ttgcgttgc 480

tagcattatc tccttgagaa aggcttcaa ttggcttta attcctcac agttcagtaa 540

ggacaaggac ccctccctt tggcattt ctgtaacgtt ttcatgaaca caaaatcttc 600

ataaagattc ctttcatctt ctatcttgc caa 633

<210> 72
<211> 885
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (29)..(808)

<400> 72

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			Met	Ile	Glu	Thr	Tyr	Ser	Gln	Thr						
			1							5						
gct	ccc	cgc	tcc	gtg	gcc	cct	gga	cca	ccc	gtc	agt	atg	aaa	att	ttt	100
Ala	Pro	Arg	Ser	Val	Ala	Pro	Gly	Pro	Pro	Val	Ser	Met	Lys	Ile	Phe	
10					15						20					
atg	tat	tta	ctt	act	gtg	ttt	ctc	atc	acc	cag	atg	att	ggg	tca	gca	148
Met	Tyr	Leu	Leu	Thr	Val	Phe	Leu	Ile	Thr	Gln	Met	Ile	Gly	Ser	Ala	
25					30					35					40	
ctc	ttt	gct	gtg	tat	ctt	cac	aga	aga	ctg	gac	aag	ata	gaa	gat	gaa	196
Leu	Phe	Ala	Val	Tyr	Leu	His	Arg	Arg	Leu	Asp	Lys	Ile	Glu	Asp	Glu	
45					50						55					
agg	aat	ctt	tat	gaa	gat	ttt	gtg	ttc	atg	aaa	aca	tta	cag	aaa	tgc	244
Arg	Asn	Leu	Tyr	Glu	Asp	Phe	Val	Phe	Met	Lys	Thr	Leu	Gln	Lys	Cys	
60					65						70					
aac	aaa	gga	gag	ggg	gcc	tta	tcc	tta	ctg	aac	tgt	gag	gaa	att	aaa	292
Asn	Lys	Gly	Glu	Gly	Ala	Leu	Ser	Leu	Leu	Asn	Cys	Glu	Glu	Ile	Lys	
75					80					85						
agc	cgg	ttt	gaa	gcc	ttt	ctc	aag	gag	ata	atg	cta	aac	aaa	gaa	acg	340
Ser	Arg	Phe	Glu	Ala	Phe	Leu	Lys	Glu	Ile	Met	Leu	Asn	Lys	Glu	Thr	
90					95					100						
aag	aaa	gaa	aaa	aat	gtt	gca	atg	caa	aaa	ggc	gac	cag	gat	cct	cga	388
Lys	Lys	Glu	Lys	Asn	Val	Ala	Met	Gln	Lys	Gly	Asp	Gln	Asp	Pro	Arg	
105					110					115				120		
gtt	gca	gca	cat	gtc	ata	agt	gag	gcc	agc	agt	agc	aca	gcg	tct	gtt	436
Val	Ala	Ala	His	Val	Ile	Ser	Glu	Ala	Ser	Ser	Ser	Thr	Ala	Ser	Val	
125					130						135					
ctc	cag	tgg	gcc	ccc	aaa	ggc	tac	tac	acc	ata	agc	agc	aac	ttg	gtg	484
Leu	Gln	Trp	Ala	Pro	Lys	Gly	Tyr	Tyr	Thr	Ile	Ser	Ser	Asn	Leu	Val	

140

145

150

acc ctc gag aac ggg aag cag ctg gcc gtt aaa aga caa gga ctc tat 532
 Thr Leu Glu Asn Gly Lys Gln Leu Ala Val Lys Arg Gln Gly Leu Tyr
 155 160 165

tat atc tac gcc caa gtc acc ttc tgt tcc aat cg gaa gct tcg agt 580
 Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser
 170 175 180

caa gct ccg ttc ata gcc agc ctc tgc ctg cat tcc ccg agt gga tcc 628
 Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu His Ser Pro Ser Gly Ser
 185 190 195 200

gag aga gtc tta ctc aga gct gca aat gcc cg agt tcc tcc aaa ccc 676
 Glu Arg Val Leu Leu Arg Ala Ala Asn Ala Arg Ser Ser Ser Lys Pro
 205 210 215

tgt ggg cag caa tcc att cac ttg gga gga gtc ttc gaa ctg cat cca 724
 Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu His Pro
 220 225 230

gg t gct tcg gtg ttc gtg aac gtg act gat ccg agc caa gtg agc cac 772
 Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His
 235 240 245

ggg acg ggc ttc acg tct ttt ggc ttg ctc aaa ctc tgaacactgg 818
 Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
 250 255 260

cacctcgca g cccgcgaggc ctgcaggccg cggctgagct cacgctggga gtcttcacaa 878
 tacagca 885

<210> 73

<211> 260

<212> PRT

<213> Felis catus

<400> 73

Met Ile Glu Thr Tyr Ser Gln Thr Ala Pro Arg Ser Val Ala Pro Gly
 1 5 10 15

Pro Pro Val Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
 20 25 30

Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg

35

40

45

Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val
 50 55 60

Phe Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser
 65 70 75 80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys
 85 90 95

Glu Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met
 100 105 110

Gln Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu
 115 120 125

Ala Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr
 130 135 140

Tyr Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu
 145 150 155 160

Ala Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe
 165 170 175

Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu
 180 185 190

Cys Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala
 195 200 205

Asn Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu
 210 215 220

Gly Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val
 225 230 235 240

Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly
 245 250 255

Leu Leu Lys Leu
 260

<210> 74

<211> 885

<212> DNA

<213> Felis catus

<400> 74

tgctgttatta tgaagactcc cagcgtgagc tcagccgcgg cctgcaggcc tcgcggcctg 60
cgaggtgcca gtgttcagag tttgagcaag ccaaaagacg tgaagcccg 120
acttggctcg gatcagtcac gttcacgaac accgaagcac ctggatgcag ttcgaagact 180
cctcccaagt gaatggattg ctgcccacag ggttggagg aactgcgggc atttgcagct 240
ctgagtaaga ctctctcgga tccactcggg gaatgcaggc agaggctggc tatgaacgga 300
gcttgactcg aagcttcccc attggaacag aaggtgactt gggcgtagat ataatagagt 360
ccttgcgttt taacggccag ctgcttcccc ttctcgaggg tcaccaagtt gctgcttatg 420
gtgttagtagc ctttgggggc ccactggaga acagacgctg tgctactgct ggcctcactt 480
atgacatgtg ctgcaactcg aggatcctgg tcgcctttt gcattgcaac attttttct 540
ttcttcgttt ctttggtag cattatctcc ttgagaaagg cttcaaaccg gcttttaatt 600
tcctcacagt tcagtaagga taaggcccc tctccttgc tgcatggc 660
aatgaacacaa aatcttcata aagattccctt tcacatctca tcttgcag tcttgcgtga 720
agatacacag caaagagtgc tgacccaatc atctgggtga tgagaaacac agtaagtaaa 780
tacataaaaaa ttttcataact gacgggtgg ccagggccca cggagcgggg agcagttgg 840
ctatatgttt cgatcatgct gtgttaaagt tgaaatggta tcttc 885

<210> 75

<211> 780

<212> DNA

<213> Felis catus

<400> 75

atgatcgaaa catatagcca aactgctccc cgctccgtgg cccctggacc acccgtcagt 60
atgaaaattt ttatgttattt acttactgtg tttctcatca cccagatgat tgggtcagca 120
ctctttgctg tgtatctca cagaagactg gacaagatag aagatgaaag gaatctttat 180
gaagattttg tgttcatgaa aacattacag aaatgcaaca aaggagaggg ggccttatcc 240

ttactgaact gtgaggaaat taaaagccgg tttgaagcct ttctcaagga gataatgcta 300
aacaaagaaa cgaagaaaga aaaaaatgtt gcaatgcaaa aaggcgacca ggatcctcga 360
gttgcagcac atgtcataaag tgaggccagc agtagcacag cgtctgtct ccagtggcc 420
cccaaaggct actacaccat aagcagcaac ttggtgaccc tcgagaacgg gaagcagctg 480
gccgttaaaa gacaaggact ctattatatc tacgcccag tcaccttctg ttccaatcgg 540
gaagcttcga gtcaagctcc gttcatagcc agcctctgcc tgcattcccc gagtggatcc 600
gagagagtct tactcagagc tgcaaattgcc cgcaagttcct ccaaaccctg tggcagcaa 660
tccattcact tgggaggagt ctgcgaactg catccaggtg cttcggtgtt cgtgaacgtg 720
actgatccga gccaagttag ccacgggacg ggcttcacgt cttttggctt gctcaaactc 780

<210> 76
<211> 780
<212> DNA
<213> *Felis catus*

<400> 76
gagtttgagc aagccaaaag acgtgaagcc cgtcccgtagg ctcacttggc tcggatcagt 60
cacgttcacg aacaccgaag cacctggatg cagttcgaag actcctccca agtgaatgg 120
ttgctgccc cagggtttgg aggaactgcg ggcatttgc gctctgagta agactctctc 180
ggatccactc gggaaatgca ggcagaggct ggctatgaac ggagcttgac tcgaagcttc 240
ccgattggaa cagaaggtga cttggcgta gatataatag agtccttgc ttttaacggc 300
cagctgcttc cgcgttcgcg gggtcaccaa gttgtgtttt atgggttagt agcctttggg 360
ggcccactgg agaacagacg ctgtgctact gctggcctca cttatgacat gtgctgcaac 420
tcgaggatcc tggtcgcctt tttgcattgc aacattttt tctttcttcg tttctttgtt 480
tagcattatc tccttgagaa aggcttcaaa ccggctttta attcctcac agttcagtaa 540
ggataaggcc cccttcctt tggcattt ctgtaatgtt ttcatgaaca caaaatctc 600
ataaaagattc ctttcatctt ctatcttgc cagtcttcg tgaagataca cagcaaagag 660
tgctgaccca atcatctggg tgatgagaaa cacagtaagt aaatacataa aaattttcat 720

actgacgggt ggtccagggg ccacggagcg gggagcagtt tggctataatg tttcgatcat 780

<210> 77

<211> 633

<212> DNA

<213> *Felis catus*

<220>

<221> CDS

<222> (1)..(633)

<400> 77

ctg gac aag ata gaa gat gaa agg aat ctt tat gaa gat ttt gtg ttc 48
Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
1 5 10 15

atg aaa aca tta cag aaa tgc aac aaa gga gag ggg gcc tta tcc tta 96
Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser Leu
20 25 30

ctg aac tgt gag gaa att aaa agc cgg ttt gaa gcc ttt ctc aag gag 144
Leu Asn Cys Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys Glu
35 40 45

ata atg cta aac aaa gaa acg aag aaa gaa aaa aat gtt gca atg caa 192
Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met Gln
50 55 60

aaa ggc gac cag gat cct cga gtt gca gca cat gtc ata agt gag gcc 240
Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu Ala
65 70 75 80

agc agt agc aca gcg tct gtt ctc cag tgg gcc ccc aaa ggc tac tac 288
Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr Tyr
85 90 95

acc ata agc agc aac ttg gtg acc ctc gag aac ggg aag cag ctg gcc 336
Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Ala
100 105 110

gtt aaa aga caa gga ctc tat tat atc tac gcc caa gtc acc ttc tgt 384
Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys
115 120 125

tcc aat cggtt gaa gct tcg agt caa gct ccg ttc ata gcc agc ctc tgc 432
Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys

130

135

140

ctg cat tcc ccg agt gga tcc gag aga gtc tta ctc aga gct gca aat 480
 Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala Asn
 145 150 155 160

gcc cgc agt tcc tcc aaa ccc tgt ggg cag caa tcc att cac ttg gga 528
 Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
 165 170 175

gga gtc ttc gaa ctg cat cca ggt gct tcg gtg ttc gtg aac gtg act 576
 Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr
 180 185 190

gat ccg agc caa gtg agc cac ggg acg ggc ttc acg tct ttt ggc ttg 624
 Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
 195 200 205

ctc aaa ctc 633
 Leu Lys Leu
 210

<210> 78
 <211> 211
 <212> PRT
 <213> Felis catus

<400> 78
 Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu Tyr Glu Asp Phe Val Phe
 1 5 10 15

Met Lys Thr Leu Gln Lys Cys Asn Lys Gly Glu Gly Ala Leu Ser Leu
 20 25 30

Leu Asn Cys Glu Glu Ile Lys Ser Arg Phe Glu Ala Phe Leu Lys Glu
 35 40 45

Ile Met Leu Asn Lys Glu Thr Lys Lys Glu Lys Asn Val Ala Met Gln
 50 55 60

Lys Gly Asp Gln Asp Pro Arg Val Ala Ala His Val Ile Ser Glu Ala
 65 70 75 80

Ser Ser Ser Thr Ala Ser Val Leu Gln Trp Ala Pro Lys Gly Tyr Tyr
 85 90 95

Thr Ile Ser Ser Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Ala

100

105

110

Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys
115 120 125

Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys
130 135 140

Leu His Ser Pro Ser Gly Ser Glu Arg Val Leu Leu Arg Ala Ala Asn
145 150 155 160

Ala Arg Ser Ser Ser Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly
165 170 175

Gly Val Phe Glu Leu His Pro Gly Ala Ser Val Phe Val Asn Val Thr
180 185 190

Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu
195 200 205

Leu Lys Leu
210

<210> 79
<211> 633
<212> DNA
<213> Felis catus

<400> 79
gagtttgagc aagccaaaag acgtgaagcc cgtcccgtagg ctcacttggc tcggatcgt 60
cacgttcacg aacaccgaag cacctggatg cagttcgaag actcctccca agtgaatgga 120
ttgctgcccc cagggtttgg aggaactgct ggcatttgca gctctgagta agactctctc 180
ggatccactc gggaaatgca ggcagaggct ggctatgaac ggagcttgac tcgaagcttc 240
ccgattggaa cagaaggtga cttggcgta gatataatag agtccttgct ttttaacggc 300
cagctgcttc ccgttctcga gggcaccaa gttgctgctt atggtgtagt agcctttggg 360
ggcccaactgg agaacagacg ctgtgctact gctggcctca cttatgacat gtgctgcaac 420
tcgaggatcc tggtcgcctt tttgcattgc aacataaaa tctttcttcg tttctttgtt 480
tagcattatac tccttgagaa aggcttcaaa ccggctttta attcctcac agttcagtaa 540

ggataaggcc cccttcctt tggtgcattt ctgtaatgtt ttcatgaaca caaaatcttc 600

ataaagattc ctttcatctt ctatcttgc cag 633

<210> 80

<211> 610

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (29)..(430)

<400> 80

caaggcaaac actgaacatt tcagagct atg aga atg ctt ctg aat ttg agt 52
Met Arg Met Leu Leu Asn Leu Ser
1 5

ttg cta gct ctt ggg gct gcc tat gtt tct gcc ttt gct gta gaa aat 100
Leu Leu Ala Leu Gly Ala Ala Tyr Val Ser Ala Phe Ala Val Glu Asn
10 15 20

ccc atg aat aga ctg gtg gca gag acc ttg aca ctg ctc tcc act cat 148
Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr Leu Ser Thr His
25 30 35 40

cga act tgg ctg ata ggc gat ggg aac ctg atg att cct act cct gaa 196
Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met Ile Pro Thr Pro Glu
45 50 55

aat aaa aat cac caa ctg tgc att aaa gaa gtt ttt cag ggt ata gac 244
Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val Phe Gln Gly Ile Asp
60 65 70

aca ttg aag aac caa act gcc cac ggg gag gct gtg gat aaa cta ttc 292
Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala Val Asp Lys Leu Phe
75 80 85

caa aac ttg tct tta ata aaa gaa cac ata gag cgc caa aaa aaa agg 340
Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu Arg Gln Lys Lys Arg
90 95 100

tgt gca gga gaa aga tgg aga gtg aca aag ttc cta gac tac ctg caa 388
Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe Leu Asp Tyr Leu Gln
105 110 115 120

gta ttt ctt ggt gta ata aac acc gag tgg aca ccg gaa agt 430

Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr Pro Glu Ser
125 130

tgagaacaaa ccggcttatt gtagtggaaat atttggaga agaatggttt tttggcgatg 490

agaatgaggg ccaaccaaca gtagggactt aatggccagt ataactaagc ttccagagaca 550

aagtaaatat ttccaggcatc ctactacttt atcacttcac acagatgaaa tatattttag 610

<210> 81

<211> 134

<212> PRT

<213> Canis familiaris

<400> 81

Met Arg Met Leu Leu Asn Leu Ser Leu Leu Ala Leu Gly Ala Ala Tyr
1 5 10 15

Val Ser Ala Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu
20 25 30

Thr Leu Thr Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly
35 40 45

Asn Leu Met Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile
50 55 60

Lys Glu Val Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His
65 70 75 80

Gly Glu Ala Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu
85 90 95

His Ile Glu Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val
100 105 110

Thr Lys Phe Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr
115 120 125

Glu Trp Thr Pro Glu Ser
130

<210> 82

<211> 610

<212> DNA

<213> Canis familiaris

<400> 82

ctcaaataata tttcatctgt gtgaagtgtat aaagtagtag gatgcctgaa atatttactt 60
tgtctctgaa gcttagttat actggccatt aagtccctac tgggggtgg ccctcattct 120
catcgccaaa aaaccattct tctccaaaat cttccactac aataagccgg tttgttctca 180
actttccgggt gtccactcggt tgggttattac accaagaaat acttgcaggt agtcttaggaa 240
cttgcact ctccatcttt ctcctgcaca ccttttttt tggcgctcta tgggttcttt 300
tattaaagac aagtttgga atagtttac cacagcctcc ccgtggcag tttggttctt 360
caatgtgtct ataccctgaa aaacttcttt aatgcacagt tggtgatttt tattttcagg 420
agtaggaatc atcaggttcc catgcctat cagccaaat cgtgagttt agagcagtgt 480
caaggtctct gccaccagtc tattcatggg attttctaca gcaaaggcag aaacataggc 540
agccccaaaga gctagcaaac tcaaatttag aagcattctc atagctctga aatgttcagt 600
gtttgccttg 610

<210> 83

<211> 402

<212> DNA

<213> Canis familiaris

<400> 83

atgagaatgc ttctgaattt gagtttgcta gctcttgggg ctgcctatgt ttctgccttt 60
gctgtagaaa atcccatgaa tagactggtg gcagagacct tgacactgct ctccactcat 120
cgaacttggc tgataggcga tggaaacctg atgattccta ctccgtaaaa taaaatcac 180
caactgtgca ttaaagaagt tttcagggt atagacacat tgaagaacca aactgcccac 240
ggggaggctg tggataaaact attccaaaac ttgtctttaa taaaagaaca catagagcgc 300
caaaaaaaaaa ggtgtgcagg agaaagatgg agagtgcacaa agttcctaga ctacctgcaa 360
gtatttcttg gtgtataaaa caccgagttt acaccggaaa gt 402

<210> 84

<211> 402

<212> DNA

<213> Canis familiaris

<400> 84

actttccgggt gtccactcgg ttttttattac accaagaaat acttgcaggt agtcttagaa 60
cttgcact ctccatcttt ctcctgcaca cttttttt tggcgctcta tgtgttcttt 120
tattaaagac aagtttgaa atagtttac cacagcctcc ccgtggcag tttggttctt 180
caatgtgtct ataccctgaa aaacttcttt aatgcacagt tggtgatttt tattttcagg 240
agtaggaatc atcaggttcc catgcctat cagccaagtt cgatgagtg agagcagtgt 300
caaggtctct gccaccagtc tattcatggg attttctaca gcaaaggcag aaacataggc 360
agccccaaaga gctagcaaac tcaaattcag aagcattctc at 402

<210> 85

<211> 345

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)...(345)

<400> 85

ttt gct gta gaa aat ccc atg aat aga ctg gtg gca gag acc ttg aca 48
Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr
1 5 10 15

ctg ctc tcc act cat cga act tgg ctg ata ggc gat ggg aac ctg atg 96
Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met
20 25 30

att cct act cct gaa aat aaa aat cac caa ctg tgc att aaa gaa gtt 144
Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val
35 40 45

ttt cag ggt ata gac aca ttg aag aac caa act gcc cac ggg gag gct 192
Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala
50 55 60

gtg gat aaa cta ttc caa aac ttg tct tta ata aaa gaa cac ata gag 240
Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu
65 70 75 80

cgc caa aaa aaa agg tgt gca gga gaa aga tgg aga gtg aca aag ttc 288
Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe
85 90 95

cta gac tac ctg caa gta ttt ctt ggt gta ata aac acc gag tgg aca 336
Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr
100 105 110

ccg gaa agt 345
Pro Glu Ser
115

<210> 86
<211> 115
<212> PRT
<213> Canis familiaris

<400> 86
Phe Ala Val Glu Asn Pro Met Asn Arg Leu Val Ala Glu Thr Leu Thr
1 5 10 15

Leu Leu Ser Thr His Arg Thr Trp Leu Ile Gly Asp Gly Asn Leu Met
20 25 30

Ile Pro Thr Pro Glu Asn Lys Asn His Gln Leu Cys Ile Lys Glu Val
35 40 45

Phe Gln Gly Ile Asp Thr Leu Lys Asn Gln Thr Ala His Gly Glu Ala
50 55 60

Val Asp Lys Leu Phe Gln Asn Leu Ser Leu Ile Lys Glu His Ile Glu
65 70 75 80

Arg Gln Lys Lys Arg Cys Ala Gly Glu Arg Trp Arg Val Thr Lys Phe
85 90 95

Leu Asp Tyr Leu Gln Val Phe Leu Gly Val Ile Asn Thr Glu Trp Thr
100 105 110

Pro Glu Ser
115

<210> 87
<211> 345
<212> DNA

<213> Canis familiaris

<400> 87

actttccgggt gtccactcggt tgtttattac accaagaaat acttgcaggt agtcttaggaa 60
ctttgtcact ctccatcttt ctcctgcaca ccttttttt tggcgctcta tgtgttcttt 120
tattaaagac aagttttgga atagtttatac cacagcctcc ccgtggcag tttggttctt 180
caatgtgtct ataccctgaa aaacttcttt aatgcacagt tggtgatttt tattttcagg 240
agtaggaatc atcaggttcc catgcctat cagccaagtt cgatgagtg agagcagtgt 300
caaggtctct gccaccagtc tattcatggg attttctaca gcaaa 345

<210> 88

<211> 166

<212> DNA

<213> Canis familiaris

<400> 88

ctcagcttag gccagcctac gacctgcctg ctcttcctc gtcctcctg cattggctct 60
gggctccatg gcgctctgggt tgactgtgggt cattgctctc acctgcctcg gtggccttgc 120
ctccccgagc cctgtgactc cctccccaaac cctcaaggag ctcatt 166

<210> 89

<211> 272

<212> DNA

<213> Canis familiaris

<400> 89

tggccttgcc tccccgagcc ctgtgactcc ctccccaaacc ctcaaggagc tcattgagga 60
gctggtaaac atcacccaga atcaggcatc cctctgcaac ggcagcatgg tgtggagcgt 120
caacctgacc gccggcatgt actgcgcagc tctagaatct ctgatcaatg tctccgactg 180
cagcgccatc caaaggaccc agaggatgt gaaagcactg tgctctaaa agcccgccgc 240
agggcagatt tccagtgaac gcagccgaga ca 272

<210> 90

<211> 278

<212> DNA

<213> Canis familiaris

<400> 90

atggcgctct ggttgactgt ggtcattgtct ctcacctgcc tcggtggcct tgccctcccc 60
agccctgtga ctccctcccc aaccctcaag gagctcattg aggagctggt caacatcacc 120
cagaatcagg catccctctg caacggcagc atggtgtgga gcgtcaacct gaccgcccggc 180
atgtactgcg cagctctaga atctctgatc aatgtctccg actgcagcgc catccaaagg 240
acccagagga tgctgaaagc actgtgctct caaaagcc 278

<210> 91

<211> 1302

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (52)..(444)

<400> 91

ctacgacctg cctgctcttc cctcgctctt cctgcattgg ctctgggctc c atg gcg 57
Met Ala
1

ctc tgg ttg act gtg gtc att gct ctc acc tgc ctc ggt ggc ctt gcc 105
Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly Leu Ala
5 10 15

tcc ccg agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag 153
Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu
20 25 30

gag ctg gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc 201
Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser
35 40 45 50

atg gtg tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta 249
Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu
55 60 65

gaa tct ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag 297
Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln
70 75 80

agg atg ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg cag att 345
Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile
85 90 95

tcc agt gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg 393
Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val
100 105 110

aaa aac ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc 441
Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe
115 120 125 130

aga tgaagcatga aaacttagca tccttatctg tagaccaga cctgaccact 494
Arg

taagttccag attcattttt ctttccgacg tcacaaattt ctttagggagg tggggggggg 554

ggagaaccat ttccctcagct gggacctcag cctgcaccgc ctgcctccat ggagctgago 614

ccagccaccc ctgccttggt gcatggggcc cagccgggtg gccctcctcc gtctgcactt 674

catcaacgct gagggaaagc actgcattcc atgactgtcc ctcctcaga gcaaagtgc 734

gcattacagt ggaggcagat atgtgtgggaa ggggtcttgc ctgtacctgg gagtggcaca 794

gacatgtttc ttcttagcct tatttattat tttgtgttat ttaaacaagt gtcttggtt 854

gtgtctgggaa cagggagtggtt cttggagctg gggcccaagt gactcgggtt tagagagtcc 914

ctggaaataa gcactgtgtg taaaattctg ctacactact gggatcctgg ggccgacaca 974

ggggacagga gaaagggtca gagatgctgc tcttgcactgc cactcagcag ctggccctca 1034

gccaaggcagt aatttattgt ttttccttgtt atttaaagtt aagaaataaa atatgttatac 1094

aaagagttaa taatatataa aagagtagcc taaaaggctg catttgggtt gtgtggccag 1154

gccggggcgg gtggggggaa ggggtgttgc actgaatgtg ctcttcact gactttgtca 1214

aactggaagc cagaaataaa gatggtgaca agagaaaaaa aaaaaaaaaa aaaaaaaaaa 1274

aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1302

<210> 92
<211> 131
<212> PRT

<213> Canis familiaris

<400> 92

Met Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly
1 5 10 15

Leu Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu
20 25 30

Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn
35 40 45

Gly Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala
50 55 60

Ala Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg
65 70 75 80

Thr Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly
85 90 95

Gln Ile Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln
100 105 110

Leu Val Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly
115 120 125

Asn Phe Arg
130

<210> 93

<211> 1302

<212> DNA

<213> Canis familiaris

<400> 93

tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt ttttctcttg 60

tcaccatctt tatttctggc ttccagtttgc acaaagtcag tgaaagagca cattcagtga 120

caacaccctc ccccccaccc gccccggcct ggccacacac accaaatgca gccttttagg 180

ctactcttct atatattttt aactctttga taacatattt tatttcttaa ctttaataac 240

aaggaaaaac aataaattac tgcttggctg agggccagct gctgagtgcc agacaagagc 300

agcatctctg accctttctc ctgtccccctg tgtcggcccc aggatccag tgaggttagca 360

gaattttaca cacagtgc ttcccccagg actctctaaa cccgagtcac tgggccccca 420
gctccaagcc actccctgtc cccagcacaa acaaagacac ttgtttaat aacacacaat 480
aataaataag gctaagaaga aacatgtctg tgccactccc aggtacagca agacccctc 540
ccacacatata ctgcctccac tgtaatgtc cacttgctc tgaggagggg acagtcatgg 600
gatgcagtgc ttccctcag cggtgatgaa gtgcagacgg aggaggccca cccggctggg 660
ccccatgcac caaggcaggg gtggctggc tcagctccat ggaggcaggc ggtgcaggct 720
gaggtcccag ctgaggaat ggttctcccc ccccccacc tccctaagaa atttgtgacg 780
tcggaaagaa aatgaatct ggaacttaag tggtcaggc tgggtctaca gataaggatg 840
ctaagtttc atgcttcatac taaaatttcc atggcgataa actccctta cataaggtag 900
caggttttc accaactgga tcacttcaat tttgggtct cggctgcgtt cactggaaat 960
ctgccctgcc gcgggctttt gagagcacag tgcttcagc atcctctggg tccttggat 1020
ggcgctgcag tcggagacat tgatcagaga ttctagagct gcgcagtaca tgccggcggt 1080
caggttgacg ctccacacca tgctgccgtt gcagagggat gcctgattct gggtgatgat 1140
gaccagctcc tcaatgagct cttgagggt tggggaggg a gtcacagggc tcggggaggc 1200
aaggccaccc aggcagggtga gagcaatgac cacagtcaac cagagcgcca tggagcccg 1260
agccaatgca ggaggagcga gggaaagagca ggcaggcgt ag 1302

<210> 94
<211> 393
<212> DNA
<213> Canis familiaris

<400> 94
atggcgctct ggttgcgtt ggtcattgtc ctcacccgtcc tcgggtggct tgcctccccg 60
agccctgtga ctccctcccc aaccctcaag gagctcatttggaggagctgggt caacatcacc 120
cagaatcagg catccctctg caacggcagc atgggtggaa gctcaacct gaccggccggc 180
atgtactgcg cagctctaga atctctgatc aatgtctccg actgcagcgc catccaaagg 240

acccagagga tgctgaaagc actgtgctct caaaagcccg cggcagggca gatttccagt 300
gaacgcagcc gagacaccaa aattgaagtg atccagttgg tgaaaaacct gctcacctat 360
gtaaggggag tttatcgcca tggaaatttc aga 393

<210> 95

<211> 393

<212> DNA

<213> Canis familiaris

<400> 95

tctgaaattt ccatggcgat aaactcccct tacataggtg agcaggttt tcaccaactg 60

gatcacttca attttggtgt ctcggctgctg ttcactggaa atctgccctg ccgcgggctt 120

ttgagagcac agtgctttca gcatcctctg ggtcctttgg atggcgctgc agtcggagac 180

attgatcaga gattcttagag ctgcgcagta catgccggcg gtcaggttga cgctccacac 240

catgctgccg ttgcagaggg atgcctgatt ctgggtgatg ttgaccagct cctcaatgag 300

ctccttgagg gttggggagg gagtcacagg gctcggggag gcaaggccac cgaggcaggt 360

gagagcaatg accacagtca accagagcgc cat 393

<210> 96

<211> 333

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(333)

<400> 96

agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag gag ctg 48
Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
1 5 10 15

gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc atg gtg 96
Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
20 25 30

tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta gaa tct 144
Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser

35

40

45

ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag agg atg 192
 Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg cag att tcc agt 240
 Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile Ser Ser
 65 70 75 80

gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg aaa aac 288
 Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn
 85 90 . 95

ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc aga 333
 Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 97

<211> 111

<212> PRT

<213> Canis familiaris

<400> 97

Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
 1 5 10 15

Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
 20 25 30

Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
 35 40 45

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
 50 55 60

Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Gln Ile Ser Ser
 65 70 75 80

Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn
 85 90 95

Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
 100 105 110

<210> 98

<211> 333
<212> DNA
<213> Canis familiaris

<400> 98
tctgaaattt ccatggcgat aaactcccct tacataggtg agcagggttt tcaccaactg 60
gatcacttca attttggtgt ctcggctgcg ttcactggaa atctgccctg ccgcgggctt 120
ttgagagcac agtgcttca gcatcctctg ggtccttgg atggcgctgc agtcggagac 180
attgatcaga gattctagag ctgcgcagta catgccggcg gtcaggttga cgctccacac 240
catgctgccg ttgcagaggg atgcctgatt ctgggtgatg ttgaccagct cctcaatgag 300
ctccttgagg gttggggagg gagtcacagg gct 333

<210> 99
<211> 1269
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (57)..(446)

<400> 99
ccagcctacg acctgcctgc tcttccctcg ctcctcctgc attggctctg ggctcc atg 59
Met 1

gcg ctc tgg ttg act gtg gtc att gct ctc acc tgc ctc ggt ggc ctt 107
Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly Leu
5 10 15

gcc tcc ccg agc cct gtg act ccc tcc cca acc ctc aag gag ctc att 155
Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile
20 25 30

gag gag ctg gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc 203
Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly
35 40 45

agc atg gtg tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct 251
Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
50 55 60 65

cta gaa tct ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc 299
Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr
70 75 80

cag agg atg ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg att 347
Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile
85 90 95

tcc agt gaa cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg 395
Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val
100 105 110

aaa aac ctg ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc 443
Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe
115 120 125

aga tgaaggcatga aaacttagca tccttatctg tagaccaga cctgaccact 496
Arg
130

taagttccag attcattttt ctttccgacg tcacaaattt ctttagggagg tggggggggg 556

ggagaaccat ttcctcagct gggacctcag cctgcaccgc ctgcctccat ggagctgagc 616

ccagccaccc ctgccttggt gcatggggcc cagccgggtg gccctcctcc gtctgcactt 676

catcaacgct gaggaaagc actgcatccc atgactgtcc ctcctcaga gcaaagtgc 736

gcattacagt ggaggcagat atgtgtgggaa ggggtcttg ctgtacctgg gagtggcaca 796

gacatgtttc ttcttagcct tatttattat tgtgtgttat ttaaacaagt gtcttggtt 856

gtgctgggaa cagggagtgg cttggagctg gggcccaagt gactcgggtt tagagagtcc 916

ctggaaataa gcactgtgtg taaaattctg ctacctcact gggatcctgg ggccgacaca 976

ggggacagga gaaagggtca gagatgctgc tcttgtctgc cactcagcag ctggccctca 1036

gccaaggcagt aatttattgt ttttccttgt atttaaagtt aagaaataaa atatgttatac 1096

aaagagttaa taatatataa aagagtagcc taaaaggctg catttgggtgt gtgtggccag 1156

gccggggcgg gtgggggggaa ggggtgtgtc actgaatgtg ctcttcact gactttgtca 1216

aactggaagc cagaaataaa gatggtgaca agagaaaaaaa aaaaaaaaaaaa aaa 1269

<210> 100

<211> 130

<212> PRT

<213> Canis familiaris

<400> 100

Met Ala Leu Trp Leu Thr Val Val Ile Ala Leu Thr Cys Leu Gly Gly
1 5 10 15

Leu Ala Ser Pro Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu
20 25 30

Ile Glu Glu Leu Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn
35 40 45

Gly Ser Met Val Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala
50 55 60

Ala Leu Glu Ser Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg
65 70 75 80

Thr Gln Arg Met Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly
85 90 95

Ile Ser Ser Glu Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu
100 105 110

Val Lys Asn Leu Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn
115 120 125

Phe Arg

130

<210> 101

<211> 1269

<212> DNA

<213> Canis familiaris

<400> 101

tttttttttt ttttttttc tcttgcacc atctttatTTT ctggcttcca gtttgacaaa 60

gtcagtgaaa gagcacatTC agtgacaaca ccctcccccc caccggcccc ggctggcca 120

cacacaccaa atgcagcctt ttaggctact cttctatata ttatTAactc tttgataaca 180

tatTTTatTTT cttaacttta aatacaagga aaaacaataa attactgctt ggctgagggc 240

cagctgctga gtggcagaca agagcagcat ctctgaccct ttctcctgTC ccctgtgtcg 300

gccccaggat cccagtgagg tagcagaatt ttacacacag tgcttattcc cagggactct 360
ctaaacccga gtcactggc ccccagctcc aagccactcc ctgtccccag cacaacaaa 420
gacacttgtt taaataacac acaataataa ataaggctaa gaagaaacat gtctgtgcca 480
ctcccaggtt cagcaagacc ccctcccaca catactgccc tccactgtaa tgctgcactt 540
tgctctgagg aggggacagt catggatgc agtgcttcc ctcagcggtt atgaagtgca 600
gacggaggag ggccacccgg ctgggccccca tgcaccaagg caggggtggc tgggctcagc 660
tccatggagg caggcggtgc aggctgaggt cccagctgag gaaatggttc tccccccccc 720
ccacctccct aagaaatttgc tgacgtcgga aagaaaaatg aatctgaaac ttaagtggc 780
aggtctgggt ctacagataa ggatgctaag ttttcatgct tcatactgaaa tttccatggc 840
gataaaactcc ctttacatag gtgagcgagg ttttccacca ctggatcaact tcaattttgg 900
tgtctcggt gcgttcactg gaaatccctg ccgcgggctt ttgagagcac agtgctttca 960
gcattcccttg ggtccctttgg atggcgctgc agtccggagac attgatcaga gattcttagag 1020
ctgcgcagta catgcggcg gtcagggttga cgctccacac catgctgccc ttgcagaggg 1080
atgcctgatt ctgggtgatg ttgaccagct cctcaatgag ctccctgagg gttggggagg 1140
gagtcacagg gtcggggag gcaaggccac cgaggcaggt gagagcaatg accacagtca 1200
accagagcgc catggagccc agagccaatg caggaggagc gagggaagag caggcaggc 1260
gtaggctgg 1269

<210> 102
<211> 390
<212> DNA
<213> Canis familiaris

<400> 102
atggcgctct ggttgactgt ggtcattgct ctcacctgccc tcgggtggcct tgcctccccc 60
agccctgtga ctccctcccc aaccctcaag gagctcatttgg aggagctggt caacatcacc 120
cagaatcagg catccctctg caacggcagc atgggtgga gcgtcaacct gaccgcccggc 180

atgtactgcg cagctctaga atctctgatc aatgtctccg actgcagcgc catccaaagg 240
acccagagga tgctgaaagc actgtgctct caaaagcccg cgccaggat ttccagtcaa 300
cgccggcggc acacccaaat tgaagtgatc cagttggta aaaacctgct cacctatgta 360
aggggagttt atcgccatgg aaatttcaga 390

<210> 103
<211> 390
<212> DNA
<213> *Canis familiaris*

<400> 103
tctgaaattt ccatggcgat aaactcccct tacataggtg agcagggttt tcaccaactg 60
gatcacttca attttggtgt ctcggctgcg ttcactggaa atccctgccc cgggctttg 120
agagcacagt gcttcagca tcctctgggt ccttggatg gcgctgcagt cggagacatt 180
gatcagagat tctagagctg cgcaatcat gcccggcgtc aggttgacgc tccacaccat 240
gctgccgttg cagagggatg cctgattctg ggtgatgttg accagctcct caatgagctc 300
cttgagggtt gggagggag tcacaggct cggggaggca aggccaccga ggcaggtgag 360
agcaatgacc acagtcaacc agagcgccat 390

<210> 104
<211> 330
<212> DNA
<213> *Canis familiaris*

<220>
<221> CDS
<222> (1)..(330)

<400> 104
agc cct gtg act ccc tcc cca acc ctc aag gag ctc att gag gag ctg 48
Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
1 5 10 15
gtc aac atc acc cag aat cag gca tcc ctc tgc aac ggc agc atg gtg 96
Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
20 25 30

tgg agc gtc aac ctg acc gcc ggc atg tac tgc gca gct cta gaa tct 144
Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
35 40 45

ctg atc aat gtc tcc gac tgc agc gcc atc caa agg acc cag agg atg 192
Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
50 55 60

ctg aaa gca ctg tgc tct caa aag ccc gcg gca ggg att tcc agt gaa 240
Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile Ser Ser Glu
65 70 75 80

cgc agc cga gac acc aaa att gaa gtg atc cag ttg gtg aaa aac ctg 288
Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn Leu
85 90 95

ctc acc tat gta agg gga gtt tat cgc cat gga aat ttc aga 330
Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
100 105 110

<210> 105

<211> 110

<212> PRT

<213> Canis familiaris

<400> 105

Ser Pro Val Thr Pro Ser Pro Thr Leu Lys Glu Leu Ile Glu Glu Leu
1 5 10 15

Val Asn Ile Thr Gln Asn Gln Ala Ser Leu Cys Asn Gly Ser Met Val
20 25 30

Trp Ser Val Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala Leu Glu Ser
35 40 45

Leu Ile Asn Val Ser Asp Cys Ser Ala Ile Gln Arg Thr Gln Arg Met
50 55 60

Leu Lys Ala Leu Cys Ser Gln Lys Pro Ala Ala Gly Ile Ser Ser Glu
65 70 75 80

Arg Ser Arg Asp Thr Lys Ile Glu Val Ile Gln Leu Val Lys Asn Leu
85 90 95

Leu Thr Tyr Val Arg Gly Val Tyr Arg His Gly Asn Phe Arg
100 105 110

<210> 106
<211> 330
<212> DNA
<213> *Canis familiaris*

<400> 106
tctgaaattt ccatggcgat aaactccct tacataggta agcagggttt tcaccaactg 60
gatcaattca attttggtgt ctcggctgcg ttcactggaa atccctgccc cgggctttg 120
agagcacagt gcttcagca tcctctgggt ccttggatg gcgctgcagt cggagacatt 180
gatcagagat tctagagctg cgcgtacat gccggcggtc aggttgacgc tccacaccat 240
gctgccgttg cagagggatg cctgattctg ggtgatgtt accagctcct caatgagctc 300
cttgagggtt ggggagggag tcacaggct 330

<210> 107
<211> 567
<212> DNA
<213> *Felis catus*

<220>
<221> CDS
<222> (1)..(567)

<400> 107
atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48
Met Ala Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15

aac tcc gtc tgc tct ctg ggc tgg gac ctg cct cag acc cac ggc ctg 96
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

gcc agc tcc tgt cag aag gac aga aat gac ttc gcc ttc ccc cag gac 192
Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
50 55 60

gtg ttt ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg 240
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val

65	70	75	80	
cac gtg acg aac cag aag atc ttc cac ttc ttc tgc aca gag gcg tcc				288
His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser				
85	90	95		
tcg tct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga				336
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly				
100	105	110		
ctt gat tgg cag ctg acc cgc ctg gaa gcc tgt gtc atg cag gag gtg				384
Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val				
115	120	125		
ggg gag gga gag gct ccc ctc acg aac gag gac tcc atc ctg agg aac				432
Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn				
130	135	140		
tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct				480
Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro				
145	150	155	160	
tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat				528
Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr				
165	170	175		
tca tca aca gcc ttg cag aaa aga tta agg agc gag aaa				567
Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys				
180	185			
<210> 108				
<211> 189				
<212> PRT				
<213> Felis catus				
<400> 108				
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys				
1	5	10	15	
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu				
20	25	30		
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro				
35	40	45		
Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp				
50	55	60		

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val
115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn
130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
180 185

<210> 109

<211> 567

<212> DNA

<213> Felis catus

<400> 109

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ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggttagaggga 120

gagtctttgg aagttagttcc tcaggatgga gtcctcggtc gtgaggggag cctctccctc 180

ccccacacctc tgcacacac aggcttccag gcgggtcagc tgccaatcaa gtcccggtca 240

gaattcctcc aggaggggtgg tggccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtgaaagatc ttctgggtcg tcacgtgcac caccgagagg gcttgggcct tgtggactg 360

gtctccacca aacacgtctt gggggaaaggc gaagtcattt ctgtccttct gacaggagct 420

ggcagggagt ctcctcattt gtcccaggag cgtcaaggcc ctcctgttca gcaggccgtg 480

ggtctgaggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccaggc 540

caccaagaag gaagagggca gcgccat 567

<210> 110

<211> 567

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(567)

<400> 110

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48

Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys

1

5

10

15

aac tcc gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg 96

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu

20

25

30

ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro

35

40

45

gcc agc tcc tgt cag aag gac agg aat gac ttc gcc ttc ccc cag gac 192

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp

50

55

60

gtg ttc ggt gga gac cag tcc cac aag gct caa gcc ctc tcg gtg gtg 240

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val

65

70

75

80

cac gtg acg aac cag gag atc ttc cac ttc ttc tgc aca gag gcg tcc 288

His Val Thr Asn Gln Glu Ile Phe His Phe Phe Cys Thr Glu Ala Ser

85

90

95

tcg tct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga 336

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Phe Cys Thr Gly

100

105

110

ctt gat cgg cag ctg acc cgc ctg gaa gcc tgt gtc gtg cag gag gtg 384

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val

115

120

125

ggg gag gga gag gct ccc ctc acg aac gag gac tcc ctc ctg agg aac 432

Gly	Glu	Gly	Glu	Ala	Pro	Leu	Thr	Asn	Glu	Asp	Ser	Leu	Leu	Arg	Asn	
130																140
tac	tac	caa	aga	ctc	tcc	ctc	tac	ctg	caa	gag	aag	aaa	tac	agc	cct	480
Tyr	Phe	Gln	Arg	Leu	Ser	Leu	Tyr	Leu	Gln	Glu	Lys	Lys	Tyr	Ser	Pro	
145																160
tgt	gcc	tgg	gag	atc	gtc	aga	gca	gaa	atc	atg	aga	tcc	ttg	tat	tat	528
Cys	Ala	Trp	Glu	Ile	Val	Arg	Ala	Glu	Ile	Met	Arg	Ser	Leu	Tyr	Tyr	
																165
																170
																175
tca	tca	aca	gcc	ttg	caa	aaa	aga	tta	agg	agc	gag	aaa				567
Ser	Ser	Thr	Ala	Leu	Gln	Lys	Arg	Leu	Arg	Ser	Glu	Lys				
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																185
<210> 111																
<211> 189																
<212> PRT																
<213> Felis catus																
<400> 111																
Met	Ala	Leu	Pro	Ser	Ser	Phe	Leu	Val	Ala	Leu	Val	Ala	Leu	Gly	Cys	
1																15
Asn	Ser	Val	Cys	Ser	Leu	Gly	Cys	Asp	Leu	Pro	Gln	Thr	His	Gly	Leu	
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																25
																30
Leu	Asn	Arg	Arg	Ala	Leu	Thr	Leu	Leu	Gly	Gln	Met	Arg	Arg	Leu	Pro	
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																40
																45
Ala	Ser	Ser	Cys	Gln	Lys	Asp	Arg	Asn	Asp	Phe	Ala	Phe	Pro	Gln	Asp	
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																55
																60
Val	Phe	Gly	Gly	Asp	Gln	Ser	His	Lys	Ala	Gln	Ala	Leu	Ser	Val	Val	
																65
																70
																75
																80
His	Val	Thr	Asn	Gln	Glu	Ile	Phe	His	Phe	Phe	Cys	Thr	Glu	Ala	Ser	
																85
																90
																95
Ser	Ser	Ala	Ala	Trp	Asn	Thr	Thr	Leu	Leu	Glu	Phe	Cys	Thr	Gly		
																100
																105
																110
Leu	Asp	Arg	Gln	Leu	Thr	Arg	Leu	Glu	Ala	Cys	Val	Val	Gln	Glu	Val	
																115
																120
																125
Gly	Glu	Gly	Glu	Ala	Pro	Leu	Thr	Asn	Glu	Asp	Ser	Leu	Leu	Arg	Asn	
																130
																135
																140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
180 185

<210> 112

<211> 567

<212> DNA

<213> *Felis catus*

<400> 112

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ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggttagaggga 120

gagtctttgg aagtagttcc tcaggaggga gtcctcggttc gtgaggggag cctctccctc 180

ccccacctcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240

gaattcctcc aggagggtgg tggatccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtgaaagatc tcctggatcg tcacgtgcac caccgagagg gcttgagcct tggatggactg 360

gtctccaccc aacacgtcct gggggaaaggc gaagtcattc ctgtccttct gacaggagct 420

ggcaggaggat ctcctcattt gtcccaggag cgtcaaggcc ctcctgttca gcaggccgtg 480

ggctgaggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccaggc 540

caccaagaag gaagaggc ggcatt 567

<210> 113

<211> 498

<212> DNA

<213> *Felis catus*

<220>

<221> CDS

<222> (1)..(498)

<400> 113

tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg	48
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr	
1 5 10 15	
ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac	96
Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp	
20 25 30	
aga aat gac ttc gcc ttc ccc cag gac gtg ttt ggt gga gac cag tcc	144
Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser	
35 40 45	
cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc	192
His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile	
50 55 60	
ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc	240
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ala Ala Trp Asn Thr	
65 70 75 80	
acc ctc ctg gag gaa ttc tgc acg gga ctt gat tgg cag ctg acc cgc	288
Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg	
85 90 95	
ctg gaa gcc tgt gtc atg cag gag gtg ggg gag gga gag gct ccc ctc	336
Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu	
100 105 110	
acg aac gag gac tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc	384
Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu	
115 120 125	
tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga	432
Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg	
130 135 140	
gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg cag aaa	480
Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Thr Ala Leu Gln Lys	
145 150 155 160	
aga tta agg agc gag aaa	498
Arg Leu Arg Ser Glu Lys	
165	

<210> 114
 <211> 166
 <212> PRT

<213> Felis catus

<400> 114

Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
20 25 30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg
85 90 95

Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
100 105 110

Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
145 150 155 160

Arg Leu Arg Ser Glu Lys
165

<210> 115

<211> 498

<212> DNA

<213> Felis catus

<400> 115

tttctcgctc cttaatcttt tctgcaaggc tggatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggttagaggga 120

gagtctttgg aagttagttcc tcaggatgga gtcctcggtc gtgaggggag cctctccctc 180

ccccacacctc tgcatgacac aggcttccag gcgggtcagc tgccaatcaa gtcccggtca 240
gaattcctcc aggaggggtgg tttccaagc agcagacgag gacgcctctg tgcagaagaa 300
gttggaaagatc ttctgggtcg tcacgtgcac caccgagagg gcttgggcct tgtggactg 360
gtctccacca aacacgtcct gggggaaaggc gaagtcattt ctgtccttct gacaggagct 420
ggcagggagt ctcctcattt gtcccaggag cgtcaaggcc ctctgttca gcaggccgtg 480
ggtctgaggc aggtcaca 498

<210> 116
<211> 498
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(498)

<400> 116
tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
1 5 10 15

ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 96
Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
20 25 30

agg aat gac ttc gcc ttc ccc cag gac gtg ttc ggt gga gac cag tcc 144
Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
35 40 45

cac aag gct caa gcc ctc tcg gtg gtg cac gtg acg aac cag gag atc 192
His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Glu Ile
50 55 60

ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 240
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ala Ala Trp Asn Thr
65 70 75 80

acc ctc ctg gag gaa ttc tgc acg gga ctt gat cgg cag ctg acc cgc 288
Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
85 90 95

ctg gaa gcc tgt gtc gtg cag gag gtg ggg gag gga gag gct ccc ctc 336
Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
100 105 110

acg aac gag gac tcc ctc ctg agg aac tac ttc caa aga ctc tcc ctc 384
Thr Asn Glu Asp Ser Leu Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
115 120 125

tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga 432
Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
130 135 140

gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg caa aaa 480
Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
145 150 155 160

aga tta agg agc gag aaa 498
Arg Leu Arg Ser Glu Lys
165

<210> 117
<211> 166
<212> PRT
<213> Felis catus

<400> 117
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
20 25 30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Glu Ile
50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
85 90 95

Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
100 105 110

Thr Asn Glu Asp Ser Leu Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
145 150 155 160

Arg Leu Arg Ser Glu Lys
165

<210> 118

<211> 498

<212> DNA

<213> Felis catus

<400> 118

tttctcgctc cttaatcttt tttgcaaggc tggatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtattc ttctcttgca ggttagaggga 120

gagtctttgg aagtagttcc tcaggaggga gtcctcggtc gtgagggag cctctccctc 180

ccccacacctcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccggtgca 240

gaattcctcc aggaggggtgg tggccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtgaaagatc tcctgggtcg tcacgtgcac caccgagagg gcttgagcct tgtggactg 360

gtctccaccg aacacgtcct gggggaaaggc gaagtcattc ctgtccttct gacaggagct 420

ggcagggagt ctccctcattt gtcccaggag cgtcaaggcc ctccgttca gcaggccgtg 480

ggtctgaggc aggtcaca 498

<210> 119

<211> 444

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (10)..(441)

<400> 119

ggatccacc atg tgg ctg cag aac ctg ctt ttc ctg ggc act gtg gtc tgc 51
 Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Thr Val Val Cys
 1 5 10

agc atc tct gca ccc acc agt tca ccc agc tct gtc act cgg ccc tgg 99
 Ser Ile Ser Ala Pro Thr Ser Ser Pro Ser Val Thr Arg Pro Trp
 15 20 25 30

caa cac gtg gat gcc atc aag gag gcc ctg agc ctt ctg aac aac agt 147
 Gln His Val Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser
 35 40 45

agt gaa ata act gct gtg atg aat gaa gca gta gaa gtc gtc tct gaa 195
 Ser Glu Ile Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu
 50 55 60

atg ttt gac cct gag gag ccg aaa tgc ctg cag act cac cta aag ctg 243
 Met Phe Asp Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu
 65 70 75

tac gag cag ggc cta cgg ggc agc ctc atc agc ctc aag gag cct ctg 291
 Tyr Glu Gln Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu
 80 85 90

aga atg atg gcc aac cat tac aag cag cac tgc ccc ctt act ccg gaa 339
 Arg Met Met Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu
 95 100 105 110

acg ccc tgt gaa acc cag act atc acc ttc aaa aat ttc aaa gag aat 387
 Thr Pro Cys Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn
 115 120 125

ctg aag gat ttt ctg ttt aac aac ccc ttt gac tgc tgg gga cca gac 435
 Leu Lys Asp Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp
 130 135 140

cag aag taa 444
 Gln Lys

<210> 120
 <211> 144
 <212> PRT
 <213> Felis catus

<400> 120
 Met Trp Leu Gln Asn Leu Leu Phe Leu Gly Thr Val Val Cys Ser Ile
 1 5 10 15

Ser Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His
20 25 30

Val Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu
35 40 45

Ile Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe
50 55 60

Asp Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met
85 90 95

Met Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro
100 105 110

Cys Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys
115 120 125

Asp Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys
130 135 140

<210> 121

<211> 444

<212> DNA

<213> Felis catus

<400> 121

ttacttctgg tctgggtcccc agcagtcaaa ggggttgtta aacagaaaaat ctttcagatt 60

ctctttgaaa tttttgaagg tgatagtctg ggtttcacag ggcgtttccg gagtaagggg 120

gcagtgctgc ttgtaatgggt tggccatcat tctcagaggc tccttgaggc tgatgaggct 180

cccccgtagg ccctgctcgt acagcttagt gtgagtcgtc aggcatttcg gctcctcagg 240

gtcaaacatt tcagagacga cttctactgc ttcattcatc acagcagtttta tttcactact 300

gttggtcaga aggctcaggg cctccttgc ggcattccacg tggccagg gccgagtgc 360

agagctgggt gaactgggtgg gtgcagagat gctgcagacc acagtgcaca gaaaaagcag 420

gttctgcagc cacatggtgg atcc 444

<210> 122
<211> 432
<212> DNA
<213> *Felis catus*

<400> 122
atgtggctgc agaacctgct tttcctggc actgtggtct gcagcatctc tgcacccacc 60
agttcaccca gctctgtcac tcggccctgg caacacgtgg atgccatcaa ggaggccctg 120
agccttctga acaacagtag taaaataact gctgtatga atgaagcagt agaagtcgtc 180
tctgaaatgt ttgaccctga ggagccgaaa tgcctgcaga ctcacctaaa gctgtacgag 240
cagggcctac gggcagcct catcagcctc aaggagcctc tgagaatgat gccaaccat 300
tacaaggcagc actgccccct tactccggaa acgcctgtg aaacccagac tatcacccctc 360
aaaaatttca aagagaatct gaaggatttt ctgttaaca accccttga ctgctggga 420
ccagaccaga ag 432

<210> 123
<211> 432
<212> DNA
<213> *Felis catus*

<400> 123
cttctggctc ggtccccagc agtcaaaggg gttttaaac agaaaatcct tcagattctc 60
tttggaaattt ttgaaggtga tagtctgggt ttcacagggc gtttccggag taagggggca 120
gtgctgcttgc taatggttgg ccatcattct cagaggctcc ttgaggctga tgaggctgcc 180
ccgtaggccc tgctcgtaca gctttaggtg agtctgcagg catttcggct cctcagggtc 240
aaacatttca gagacgactt ctactgcttc attcatcaca gcagttattt cactactgtt 300
gttcagaagg ctcagggcct cttgtatggc atccacgtgt tgccagggcc gagtgacaga 360
gctgggtgaa ctgggtggtg cagagatgct gcagaccaca gtgcccagga aaagcagggtt 420
ctgcagccac at 432

<210> 124

<211> 381
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(381)

<400> 124

gca ccc acc agt tca ccc agc tct gtc act cg^g ccc tgg caa cac g^tg^g 48
Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His Val
1 5 10 15

gat gcc atc aag gag gcc ctg agc ctt ctg aac aac agt agt gaa ata 96
Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu Ile
20 25 30

act gct gtg atg aat gaa gca gta gaa gtc gtc tct gaa atg ttt gac 144
Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe Asp
35 40 45

cct gag gag ccg aaa tgc ctg cag act cac cta aag ctg tac gag cag 192
Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu Gln
50 55 60

ggc cta cg^g ggc agc ctc atc agc ctc aag gag cct ctg aga atg atg 240
Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met Met
65 70 75 80

gcc aac cat tac aag cag cac tgc ccc ctt act ccg gaa acg ccc tgt 288
Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro Cys
85 90 95

gaa acc cag act atc acc ttc aaa aat ttc aaa gag aat ctg aag gat 336
Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys Asp
100 105 110

ttt ctg ttt aac aac ccc ttt gac tgc tgg gga cca gac cag aag 381
Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys
115 120 125

<210> 125
<211> 127
<212> PRT
<213> Felis catus

<400> 125

Ala Pro Thr Ser Ser Pro Ser Ser Val Thr Arg Pro Trp Gln His Val
1 5 10 15

Asp Ala Ile Lys Glu Ala Leu Ser Leu Leu Asn Asn Ser Ser Glu Ile
20 25 30

Thr Ala Val Met Asn Glu Ala Val Glu Val Val Ser Glu Met Phe Asp
35 40 45

Pro Glu Glu Pro Lys Cys Leu Gln Thr His Leu Lys Leu Tyr Glu Gln
50 55 60

Gly Leu Arg Gly Ser Leu Ile Ser Leu Lys Glu Pro Leu Arg Met Met
65 70 75 80

Ala Asn His Tyr Lys Gln His Cys Pro Leu Thr Pro Glu Thr Pro Cys
85 90 95

Glu Thr Gln Thr Ile Thr Phe Lys Asn Phe Lys Glu Asn Leu Lys Asp
100 105 110

Phe Leu Phe Asn Asn Pro Phe Asp Cys Trp Gly Pro Asp Gln Lys
115 120 125

<210> 126

<211> 381

<212> DNA

<213> Felis catus

<400> 126

cttctggct ggtccccagc agtcaaaggg gttgttaaac agaaaatcct tcagattctc 60

tttggaaattt ttgaaggta tagtctgggt ttcacagggc gtttccggag taagggggca 120

gtgctgctt taatggttgg ccatcattct cagaggctcc ttgaggctga tgaggctgcc 180

ccgttaggccc tgctcgtaca gctttaggtg agtctgcagg catttcggct cctcagggtc 240

aaacatttca gagacgactt ctactgcttc attcatcaca gcagttattt cactactgtt 300

gttcagaagg ctcagggcct ccttgatggc atccacgtgt tgccagggcc gagtgacaga 360

gctgggtgaa ctgggggtg c 381

<210> 127

<211> 28

<212> DNA
<213> Artificial Sequence

<400> 127
cctcggaggatt cagctttcaa tgcctgta

28

<210> 128
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 128
tgcccrstcg gcttcttctc c

21

<210> 129
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 129
cgactctctt trccrtcctc ctg

23

<210> 130
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 130
cctcaaattg cggcacatgt c

21

<210> 131
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 131
ctgttcagag tttgagtaag cc

22

<210> 132
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 132
gaagataccat tttcaacttt aacacagc

28

<210> 133
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 133
tgctgtattt gtaagactcc cagc

24

<210> 134
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 134
atgcactttc tttgcc

16

<210> 135
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 135
ctggagggaaa akacttcrat gattctgata tctgaaatat 42

<210> 136
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 136
ctgacycttk sttggscctc attctca 27

<210> 137
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 137
gggctcgaga aaagatttgc tgttagaaaat cccatg 36

<210> 138
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Primer

<400> 138
cccgccggccg ctcaactttc cggtgtccac tc 32

<210> 139
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 139
gtcmtggctc tyrcttgctt tgg 23

<210> 140
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 140
aaastgggcy acytcgattt tgg 23

<210> 141
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 141
gtgatgttgm ycagctcctc 20

<210> 142
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 142

aatttaaccct cactaaaggg

20

<210> 143

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 143

atggcgctct ggttgactgt

20

<210> 144

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 144

ggctttgag agcacagtgc

20

<210> 145

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 145

ccccatatga gccctgtgac tccctcccc

29

<210> 146
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 146
ggggaaattct catctgaaat ttccatggcg

30

<210> 147
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 147
atggcgctgc cctcttcctt cttg

24

<210> 148
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 148
tcatttctcg ctccttaatc ttttctgc

28

<210> 149
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 149
cagggatcca ccatgtggct gcagaacctg cttttcc

37

<210> 150
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 150
ttacttctgg tctggtcccc agcagtcaaa ggggttgtta aacagaaaaat

50

<210> 151
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 151
cacagyccca tctcctcc

18

<210> 152
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 152
gtaatacgcac tcactatagg gc

22

<210> 153
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 153

acggaattcg agatgatagt gctggc

26

<210> 154

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 154

gtgtctagat ttggtagaaa aggatgat

28

<210> 155

<211> 567

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(567)

<400> 155

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15

aac tcc gtc tgc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg 96
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

gcc agc tcc tgt cag aag gac aga agt gac ttc gcc ttc ccc cag gac 192
Ala Ser Ser Cys Gln Lys Asp Arg Ser Asp Phe Ala Phe Pro Gln Asp
50 55 60

gtg ttt ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg 240
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

cac gtg acg aac cag aag atc ttc cac ttc tgc aca gag gcg tcc 288
His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

' tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga 336
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Phe Cys Thr Gly
100 105 110

ctt gat tgg cag ctg acc cgc ctg gaa gcc tgt gtc atg cag gag gtg 384
Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val
115 120 125

ggg gag gga gag gct ccc ctc acg aac gag gac tcc atc ctg agg aac 432
Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn
130 135 140

tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct 480
Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
145 150 155 160

tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat 528
Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
165 170 175

tca tca aca gcc ttg cag aaa aga tta agg agc gag aaa 567
Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
180 185

<210> 156
<211> 189
<212> PRT
<213> Felis catus

<400> 156
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Ser Asp Phe Ala Phe Pro Gln Asp
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

Leu Asp Trp Gln Leu Thr Arg Leu Glu Ala Cys Val Met Gln Glu Val
115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn
130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
180 185

<210> 157

<211> 567

<212> DNA

<213> Felis catus

<400> 157

tttctcgctc cttaatcttt tctgcaaggc tgttgatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcggtc gtgagggag cctctccctc 180

ccccacacctcc tgcacatgacac aggcttccag gcgggtcagc tgccaaatcaa gtcccgtgca 240

gaattcctcc aggaggggtgg tgttccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtgaaagatc ttctgggtcg tcacgtgcac caccgagagg gcttgggcct tggggactg 360

gtctccacca aacacgtcct gggggaaaggc gaagtcactt ctgtccttct gacaggagct 420

ggcagggagt ctcctcattt gtcccaggag cgtcaaggcc ctcctgttca gcaggccgtg 480

ggtctgagggc aggtcacagc ccagagagca gacggagttg cagcccagcg ccaccagggc 540

caccaagaag gaagagggca gcgccat 567

<210> 158

<211> 498

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(498)

<400> 158

tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
1 5 10 15

ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 96
Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
20 25 30

aga agt gac ttc gcc ttc ccc cag gac gtg ttt ggt gga gac cag tcc 144
Arg Ser Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
35 40 45

cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc 192
His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
50 55 60

ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 240
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ala Ala Trp Asn Thr
65 70 75 80

acc ctc ctg gag gaa ttc tgc acg gga ctt gat tgg cag ctg acc cgc 288
Thr Leu Leu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg
85 90 95

ctg gaa gcc tgt gtc atg cag gag gtg ggg gag gga gag gct ccc ctc 336
Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
100 105 110

acg aac gag gac tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc 384
Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
115 120 125

tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga 432
Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
130 135 140

gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg cag aaa 480
Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
145 150 155 160

aga tta agg agc gag aaa 498
Arg Leu Arg Ser Glu Lys
165

<210> 159
<211> 166
<212> PRT
<213> Felis catus

<400> 159
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
20 25 30

Arg Ser Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Trp Gln Leu Thr Arg
85 90 95

Leu Glu Ala Cys Val Met Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
100 105 110

Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys

145

150

155

160

Arg Leu Arg Ser Glu Lys
165

<210> 160

<211> 498

<212> DNA

<213> *Felis catus*

<400> 160

tttctcgctc cttaatcttt tctgcaaggc tggatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggtagaggga 120

gagtctttgg aagttagttcc tcaggatgga gtcctcggtc gtgaggggag cctctccctc 180

ccccacacctcc tgcatgacac aggcttccag gcgggtcagc tgccaatcaa gtcccgtgca 240

gaattcctcc aggaggggtgg tggccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtgaaagatc ttctggttcg tcacgtgcac caccgagagg gcttggcct tggactg 360

gtctccacca aacacgtcct ggggaaggc gaagtcactt ctgtccttct gacaggagct 420

ggcaggaggt ctccatatt gtcccaggag cgtcaaggcc ctccgttca gcaggccgtg 480

ggtctgagggc aggtcaca 498

<210> 161

<211> 582

<212> DNA

<213> *Felis catus*

<220>

<221> CDS

<222> (1)..(582)

<400> 161

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48

Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys

1

5

10

15

1 aac tcc gtc tct ctg ggc tgt gat ctg cct cag acc cac ggc ctg 96

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu

20

25

30

ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct	144
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro	
35 40 45	
gcc agc tcc tgt cag aag gac aga agt gac ttc gcc ttc ccc cag gac	192
Ala Ser Ser Cys Gln Lys Asp Arg Ser Asp Phe Ala Phe Pro Gln Asp	
50 55 60	
gtg ttc ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg	240
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val	
65 70 75 80	
cac gtg acg aac cag aag atc ttc cac ttc tgc aca gag gcg tcc	288
His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser	
85 90 95	
tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga	336
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly	
100 105 110	
ctt gat cgg cag ctg acc cgc ctg gaa gcc tgt gtc gtg cag gag gtg	384
Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val	
115 120 125	
ggg gag gga gag gct ccc ctg acg aac gag gac att cat ccc gag gac	432
Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp	
130 135 140	
tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc tac ctg caa gag	480
Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu	
145 150 155 160	
aag aaa tac agc cct tgt gcc tgg gag atc gtc aga gca gaa atc atg	528
Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met	
165 170 175	
aga tcc ttg tat tat tca tca aca gcc ttg cag aaa aga tta agg agc	576
Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser	
180 185 190	
gag aaa	582
Glu Lys	

<210> 162
 <211> 194
 <212> PRT

<213> Felis catus

<400> 162

Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Ser Asp Phe Ala Phe Pro Gln Asp
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val
115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ile His Pro Glu Asp
130 135 140

Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu
145 150 155 160

Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met
165 170 175

Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser
180 185 190

Glu Lys

<210> 163

<211> 582

<212> DNA

<213> Felis catus

<400> 163

tttctcgctc cttaatcttt tctgcaaggc tggtgatgaa taatacaagg atctcatgat 60
ttctgctctg acgatctccc aggcacaagg gctgtattc ttctcttgcg ggtagaggga 120
gagtctttgg aagtagttcc tcaggatgga gtcctcgaaa tgaatgtcct cggtcgtag 180
gggagcctct ccctccccca cctcctgcac gacacaggct tccaggcgaa tcagctgccc 240
atcaagtccc gtgcagaatt cctccaggag ggtgggttc caagcagcag acgaggacgc 300
ctctgtgcag aagaagtggaa agatcttctg gttcgtaacg tgcaccaccc agagggctt 360
ggccttggg gactggtctc caccgaacac gtcctggggg aaggcgaagt cacttctgtc 420
cttctgacag gagctggcag ggagtctccc catttgcacca aggagcgtca aggcctcc 480
gttcagcagg ccgtgggtct gaggcagatc acagcccaga gagcagacgg agttgcagcc 540
cagcgccacc agggccacca agaaggaaga gggcagcgcc at 582

<210> 164

<211> 513

<212> DNA

<213> *Felis catus*

<220>

<221> CDS

<222> (1)..(513)

<400> 164

tgt gat ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
1 5 10 15

ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgt cag aag gac 96
Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp
20 25 30

aga agt gac ttc gcc ttc ccc cag gac gtg ttc ggt gga gac cag tcc 144
Arg Ser Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
35 40 45

cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc 192
His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
50 55 60

ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc	240		
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr			
65 70 75 80			
acc ctc ctg gag gaa ttc tgc acg gga ctt gat cgg cag ctg acc cgc	288		
Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg			
85 90 95			
ctg gaa gcc tgt gtc gtg cag gag gtg ggg gag gga gag gct ccc ctg	336		
Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu			
100 105 110			
acg aac gag gac att cat ccc gag gac tcc atc ctg agg aac tac ttc	384		
Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr Phe			
115 120 125			
caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct tgt gcc	432		
Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala			
130 135 140			
tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat tca tca	480		
Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser			
145 150 155 160			
aca gcc ttg cag aaa aga tta agg agc gag aaa	513		
Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys			
165 170			
<210> 165			
<211> 171			
<212> PRT			
<213> Felis catus			
<400> 165			
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr			
1 5 10 15			
Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp			
20 25 30			
Arg Ser Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser			
35 40 45			
His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile			
50 55 60			
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ala Ala Trp Asn Thr			

65

70

75

80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
85 90 95

Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
100 105 110

Thr Asn Glu Asp Ile His Pro Glu Asp Ser Ile Leu Arg Asn Tyr Phe
115 120 125

Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala
130 135 140

Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser
145 150 155 160

Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
165 170

<210> 166

<211> 513

<212> DNA

<213> Felis catus

<400> 166

tttctcgctc cttaatcttt tctgcaaggc tggatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggttagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcgaaa tgaatgtcct cgttcgtag 180

gggagcctct ccctccccca cctcctgcac gacacaggct tccaggcggg tcagctgccg 240

atcaagtccc gtgcagaatt cctccaggag ggtgggttc caagcagcag acgaggacgc 300

ctctgtgcag aagaagtggc agatcttctg gttcgacacg tgcaccaccc agagggcttg 360

ggccttgg gactggcttc caccgaacac gtcctgggg aaggcgaagt cacttctgtc 420

cttctgacag gagctggcag ggagtctccc catttgcctt aggagcgtca agggccctcct 480

gttcagcagg ccgtgggtct gaggcagatc aca 513

<210> 167

<211> 567

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(567)

<400> 167

atg gcg ctg ccc tct tcc ttc ttg gtg gcc ctg gtg gcg ctg ggc tgc 48
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15

aac tct gtc tct ctg ggc tgt gac ctg cct cag acc cac ggc ctg 96
Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

ctg aac agg agg gcc ttg acg ctc ctg gga caa atg agg aga ctc cct 144
Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

gcc agc tcc tgc cag aag gac aga aat gac ttc gcc ttc ccc cag gac 192
Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
50 55 60

gtg ttc ggt gga gac cag tcc cac aag gcc caa gcc ctc tcg gtg gtg 240
Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

cac gtg acg aac cag aag atc ttc cac ttc tgc aca gag gcg tcc 288
His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

tcg tct gct gct tgg aac acc acc ctc ctg gag gaa ttc tgc acg gga 336
Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Phe Cys Thr Gly
100 105 110

ctt gat cgg cag ctg acc cgc ctg gaa gcc tgt gtc gtg cag gag gtg 384
Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val
115 120 125

ggg gag gga gag gct ccc ctc acg aac gag gac tcc atc ctg agg aac 432
Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn
130 135 140

tac ttc caa aga ctc tcc ctc tac ctg caa gag aag aaa tac agc cct 480
Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
145 150 155 160

tgt gcc tgg gag atc gtc aga gca gaa atc atg aga tcc ttg tat tat 528
Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
165 170 175

tca tca aca gcc ttg cag aaa aga tta agg agc gag aaa 567
Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
180 185

<210> 168
<211> 189
<212> PRT
<213> Felis catus

<400> 168
Met Ala Leu Pro Ser Ser Phe Leu Val Ala Leu Val Ala Leu Gly Cys
1 5 10 15

Asn Ser Val Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Gly Leu
20 25 30

Leu Asn Arg Arg Ala Leu Thr Leu Leu Gly Gln Met Arg Arg Leu Pro
35 40 45

Ala Ser Ser Cys Gln Lys Asp Arg Asn Asp Phe Ala Phe Pro Gln Asp
50 55 60

Val Phe Gly Gly Asp Gln Ser His Lys Ala Gln Ala Leu Ser Val Val
65 70 75 80

His Val Thr Asn Gln Lys Ile Phe His Phe Phe Cys Thr Glu Ala Ser
85 90 95

Ser Ser Ala Ala Trp Asn Thr Thr Leu Leu Glu Glu Phe Cys Thr Gly
100 105 110

Leu Asp Arg Gln Leu Thr Arg Leu Glu Ala Cys Val Val Gln Glu Val
115 120 125

Gly Glu Gly Glu Ala Pro Leu Thr Asn Glu Asp Ser Ile Leu Arg Asn
130 135 140

Tyr Phe Gln Arg Leu Ser Leu Tyr Leu Gln Glu Lys Lys Tyr Ser Pro
145 150 155 160

Cys Ala Trp Glu Ile Val Arg Ala Glu Ile Met Arg Ser Leu Tyr Tyr
165 170 175

Ser Ser Thr Ala Leu Gln Lys Arg Leu Arg Ser Glu Lys
180 185

<210> 169

<211> 567

<212> DNA

<213> *Felis catus*

<400> 169

tttctcgctc cttaatcttt tctgcaaggc tggatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggttagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcggtc gtgagggag cctctccctc 180

ccccacacctcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240

gaattcctcc aggaggggtgg tggccaagc agcagacgag gacgcctctg tgcagaagaa 300

gttggaaagatc ttctgggtcg tcacgtgcac caccgagagg gcttgggcct tggactg 360

gtctccaccg aacacgtcct gggggaaaggc gaagtcattt ctgtccttct ggcaggagct 420

ggcagggagt ctccctcattt gtcccaggag cgtcaaggcc ctccctgttca gcaggccgtg 480

ggctgaggc aggtcacagc ccagagagca gacagagttt cagccagcg ccaccaggc 540

caccaagaag gaagagggca ggcacat 567

<210> 170

<211> 498

<212> DNA

<213> *Felis catus*

<220>

<221> CDS

<222> (1)..(498)

<400> 170

tgt gac ctg cct cag acc cac ggc ctg ctg aac agg agg gcc ttg acg 48

Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr

1

5

10

15

ctc ctg gga caa atg agg aga ctc cct gcc agc tcc tgc cag aag gac 96

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp

20

25

30

aga aat gac ttc gcc ttc ccc cag gac gtg ttc ggt gga gac cag tcc 144
Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
35 40 45

cac aag gcc caa gcc ctc tcg gtg gtg cac gtg acg aac cag aag atc 192
His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
50 55 60

ttc cac ttc ttc tgc aca gag gcg tcc tcg tct gct gct tgg aac acc 240
Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ala Ala Trp Asn Thr
65 70 75 80

acc ctc ctg gag gaa ttc tgc acg gga ctt gat cgg cag ctg acc cgc 288
Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
85 90 95

ctg gaa gcc tgt gtc gtg cag gag gtg ggg gag gga gag gct ccc ctc 336
Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Ala Pro Leu
100 105 110

acg aac gag gac tcc atc ctg agg aac tac ttc caa aga ctc tcc ctc 384
Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
115 120 125

tac ctg caa gag aag aaa tac agc cct tgt gcc tgg gag atc gtc aga 432
Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
130 135 140

gca gaa atc atg aga tcc ttg tat tat tca tca aca gcc ttg cag aaa 480
Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
145 150 155 160

aga tta agg agc gag aaa 498
Arg Leu Arg Ser Glu Lys
165

<210> 171
<211> 166
<212> PRT
<213> Felis catus

<400> 171
Cys Asp Leu Pro Gln Thr His Gly Leu Leu Asn Arg Arg Ala Leu Thr
1 5 10 15

Leu Leu Gly Gln Met Arg Arg Leu Pro Ala Ser Ser Cys Gln Lys Asp

20

25

30

Arg Asn Asp Phe Ala Phe Pro Gln Asp Val Phe Gly Gly Asp Gln Ser
 35 40 45

His Lys Ala Gln Ala Leu Ser Val Val His Val Thr Asn Gln Lys Ile
 50 55 60

Phe His Phe Phe Cys Thr Glu Ala Ser Ser Ser Ala Ala Trp Asn Thr
 65 70 75 80

Thr Leu Leu Glu Glu Phe Cys Thr Gly Leu Asp Arg Gln Leu Thr Arg
 85 90 95

Leu Glu Ala Cys Val Val Gln Glu Val Gly Glu Gly Glu Ala Pro Leu
 100 105 110

Thr Asn Glu Asp Ser Ile Leu Arg Asn Tyr Phe Gln Arg Leu Ser Leu
 115 120 125

Tyr Leu Gln Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Ile Val Arg
 130 135 140

Ala Glu Ile Met Arg Ser Leu Tyr Tyr Ser Ser Thr Ala Leu Gln Lys
 145 150 155 160

Arg Leu Arg Ser Glu Lys
 165

<210> 172

<211> 498

<212> DNA

<213> Felis catus

<400> 172

tttctcgctc cttaatcttt tctgcaaggc tggatgaa taatacaagg atctcatgat 60

ttctgctctg acgatctccc aggcacaagg gctgtatttc ttctcttgca ggttagaggga 120

gagtctttgg aagtagttcc tcaggatgga gtcctcggtc gtgaggggag cctctccctc 180

ccccacacctcc tgcacgacac aggcttccag gcgggtcagc tgccgatcaa gtcccgtgca 240

gaattcctcc aggaggggtgg tggccaagc agcagacgag gacgcctctg tgcagaagaa 300

gtgaaagatc ttctgggtcg tcacgtgcac caccgagagg gcttgggcct tggactg 360

gtctccaccc aacacgtcct ggggaaaggc gaagtcattt ctgtccttct ggcaggagct 420

ggcaggaggat ctcctcattt gtcccaggag cgtcaaggcc ctccgttca gcaggccgtg 480

ggtctgaggc aggtcaca 498

<210> 173

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 173

attaggatcc atggcgctgc cctttccct 29

<210> 174

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 174

gcctctagac tgtcatttct cgctccttaa tctttctgc 40